July 16, 2001, 16:35:41; Search time 56.06 Seconds (without alignments) 12.977 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-09-786-648-3 62 Title: Perfect score: Sequence:

1 VEVPGSQHIDSQ 12

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

412676 seqs, 60623988 residues Searched:

412676 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseqfyaeneseqp/AA1985.DAT:*
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/SIDSB/gcgdata/geneseqfyaeneseqp/AA1989.DAT:* 13: 114: 115: 117: 118: 220: 221: Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Ouery Match Length DB ID	DB	a	Description
-	62	100.0	12	21	AAY87461	Cholera toxin B/en
7	62	100.0	15	10	AAP93498	CTP3 epitope of th
٣	62	100.0	15	16	AAR85125	Cholera toxin B an
4	62	100.0	21	21	AAY87462	Cholera toxin B/en
2	62	100.0	21	21	AAY87463	E. coli heat labil
9	62	100.0	23	16	AAR76748	Residues 50-64 of
7	62	100.0	26	4	AAP30265	Sequence of amino
80	62	100.0	41	ဖ	AAP50439	Network polymer wh
6	62	100.0	46	9	AAP50436	Network polymer wh
10	62	100.0	47	4	AAP30600	Sequence of amino
11	62	100.0	93	16	AAR72545	ADP-ribosylating t

Escherichia coli v	E. coli heat-labil	Heat labile toxin	E coli verotoxin-1	Sequence of sub-un	Synthetic cholera	Heat labile entero	Cholera toxin B su	Cholera toxin B su	Amino acid sequenc	Cholera Toxin B-su	B subunit of the h	Cholera toxin B su	Amino acid sequenc	Plant-optimized E.	Plant-optimized V.	GtfB.1/CTB chimeri	LTB-CTB fusion pro		Sequence of LT-B-M	Recombinant exotox	Recombinant exotox	Recombinant exotox	LTB-CTP fusion pro	Labile toxin (LT-B	C. jejuni flagelli	HSV-1 antigen/heat	B subunit of CT.		Helicobacter pylor	Helicobacter pylor	Adhesin/CTXA2B chi	Cholera toxin B su	Bovine rotavirus V
AAY41816	AAW95226	AAY68365	AAB66239	AAP50340	AAW04857	AAR94939	AAW06606	AAW06607	AAW80808	AAR04163	AAP93561	AAW06605	AAW59770	AAY96652	AAY96872	AAR12630	AAR04825	AAB73241	AAR50227	AAB73242	AAB73243	AAB73244	AAW94082	AAY01300	AAW67443	AAR11272	AAR28831	AAW74466	AAW80599	AAW80600	AAY32094	AAB15525	AAB15526
20	20	21	22	9	17	17	17	17	19	11	10	17	19	21	21	12	11	22	15	22	22	22	20	20	20	12	13	19	19	19	20	21	21
93	93	93	66	103	103	103	103	103	103	118	124	124	124	124	124	126	131	134	138	142	155	163	170	371	371	405	124	461	749	1338	461	15	15
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.3	90.3	90.3	90.3	79.0	75.8	75.8
62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	. 29	62	62	62	62	62	62	62	62	62	62	62	26	26	99	26	49	47	47
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY87461 standard; peptide; 12 AA. AAY87461; RESULT AAY87461

03-JUL-2000 (first entry)

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:3.

EtxB; Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Vibrio cholerae. Escherichia coli.

WO200014114-A1.

16-MAR-2000

99WO-GB02970. 07-SEP-1999; 98GB-0019484. 07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ -

0; Gaps

Indels

Score 62; DB 10; Pred. No. 4.1e-05; Mismatches 0;

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100.0%;

15 AA;

Length 15;

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oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immuno-
subunit. The DNA sequence encoding this ligates to othersynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                     Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen; intestines; secretory; IgA class.
                                                                                                                                                                                                                                                                                                                                                                                          Cholera toxin B antigenic peptide fragment CTP3.
                                                                                                                                                                                                                                                                                              AAR85125 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YEDA ) YEDA RES & DEV CO LID.
                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                    1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9529701-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                           13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marks RS,
                                                                             Seguence
                                                                                                                                                                                                                                                                                                                             AAR85125;
                                              therapy
                                                                                                                                                                                                                                                                                AAR85125
                                                                                                                                                                                                                                                                RESULT
 8888888
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                                     The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous from vibrio collerae which do not bind to the ubiquitous composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the through GM-1 binding. The peptides of the invention are fragments of the cornal EtxB and CtxB, except that they do not bind or cross link GM-1. They may also be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea.

They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. In medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. In medicine as an immunomodulator or adjuvant. They may encounting and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholera toxin B subunit; flagellin fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 62; DB 21; Length 12; Best Local Similarity 100.0%; Pred. No. 3.2e-05; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTP3 epitope of the Cholera toxin B subunit.
              Disclosure; Page 15; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP93498 standard; protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89WO-US01932,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTP3 epitope of Cholera to vaccine; immunotherapy; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                           particularly preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 vevpgsghidsg 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                          12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO8910967-A.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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(first entry)

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                                                      Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                                                         A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and esp. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 62; DB 16;
100.0%; Pred. No. 4.1e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                      Claim 7; Page 25; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
WPI; 1995-403805/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secretory IgA class.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                             aldehyde silica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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New recombinant flagellin gene including sequence – for heterologous epitope, and expressed fusion proteins, useful in vaccines and for prodn.

New recombinant flagellin

antibodies.

Newton SMC;

Marjarian WR, Stocker BAD,

WPI; 1989-356496/48

N-PSDB; AAN92414

(PRAX-) PRAXIS BIOLOGICS INC. (STRD) LEYLAND STANDFORD JUNIOR UNIV.

88US-0190570

05-MAY-1988;

This sequence corresponds to the CTP3 epitope of the Cholera toxin B

Disclosure; fig.4B; 137pp; English.

Sela M;

Mirelman D,

94IL-0109519.

1 vevpgsqhidsq 12

qq

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The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous (M-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (AbP) Abpribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the cormal EtxB and Ctx, it has been found that certain effects of the toxins, such as immunomodulation are fragments of the cormal EtxB and CtxB exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. In the preferred peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAV87460-Y87463 represent preferred peptides of the invention, AAY87460 being
                                                                                                                                                                                                Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Derivatives of Escherichia coli heat labile enterotoxins useful a immunomodulators and for treating diarrhea and which do not bind glycolipid receptor {\tt GM-1} .
                                                                                                                                                       Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 15; 62pp; English
                    AAY87462 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB02970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98GB-0019484.
                                                                                                           03-JUL-2000 (first entry)
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams NA, Hirst TR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-256943/22.
                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AA;
                                                                                                                                                                                                                                                                                     Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                     WO200014114-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000
                                                                  AAY87462;
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AAY87462
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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

98GB-0019484.

07-SEP-1998; 07-SEP-1999; 16-MAR-2000

(UYBR-) UNIV BRISTOL.

WPI; 2000-256943/22.

Williams NA,

Disclosure; Page 15; 62pp; English.

Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Escherichia coli. WO200014114-A1.

E. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5

(first entry)

03-JUL-2000

AAY87463;

AAY87463 standard; peptide; 21 AA.

RESULT AAY87463

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The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from vibrio cholerae which do not bind to the ublanitous (H-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the chrough GM-1 binding. The peptides of the invention are fragments of the Deta-4 alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea.

Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AXURT460-YR463 immunome disorder and/or toxin-induced diarrhoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent preferred peptides of the invention, AAY87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 62; DB 21;
100.0%; Pred. No. 5.9e-05;
iive 0; Mismatches 0;
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Matches 12; Conservative
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RESULT AAR76748

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Gaps

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100.0%; Score 62; DB 21; Length 21; 100.0%; Pred. No. 5.9e-05; Ive 0; Mismatches 0; Indels

1 VEVPGSQHIDSQ 12

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5 vevpgsghidsg 16

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AAR76748 standard; Protein; 23 AA

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Sequence of amino acids 50-75 of the cholera toxin Bl subunit which carries an Arg at posns. 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                    Cholera vaccine; therapy; E.coli infection; enterotoxin
                                                                       AAP30265 standard; Protein; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                         (CNRS ) CNRS CENT NAT RECH SCI. (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 11; 13pp; French
                                                                                                                              21-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Milhaud G, Raulais D, 1
Guyongruaz A, Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1983-834645/49.
                                                                                                                                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                              26-MAY-1982;
                                                                                                                                                                                                                                                                                                                   26-MAY-1983;
                                                                                                                                                                                                                                                                                         30-NOV-1983.
                                                                                                                                                                                                                                                            EP95426-A.
                                                                                                   AAP30265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is encoded by a fragment of the the plasmid pLPA93
which was used in the production of fimH fusion genes comprising
the cholera toxin B subunit inserted into the fimH gene. This insert
shows the inclusion of the B subunit into the FimH protein at position
224-226. The chimeric genes were then opt. further modified by insertion
of the hepatitis B virus surface antigen pre-S2 region into a different
of the hepatitis B virus surface antigen pre-S2 region into a different
position of the FimH adhesin of type I fimbriae. Restiction site handles
(BgllI-sites) were introduced into the fimH gene, and the foreign
epitopes are then inserted in frame. In the selected positions the
insertion of the Pithepes did not significantly alter the adhesive
function of the FimH protein. The expression of the chimeric proteins
on the surface of fimbriae on bacterial hosts illustrated the possibility
of using bacterial adhesins as general presenters of foreign antigens and
epitopes. These chimeric genes may be used in the production of variant
FinH adhesins which may be useful for targetting active compounds
and problem is a properties of protein to which
                                                                                                               FimH; type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue; FimA; FimF; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor specific bacterial adhesins - useful for targetting active compounds and microbial cells to locations of receptors
                                                                                   Residues 50-64 of cholera toxin B subunit and FimH 224-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sokurenko EV;
                                                                                                                                                                                                                                                                          5..19
/note= "Cholera toxin B subunit 50-64"
                                                                                                                                                                                                                               'note= "Represents FimH residue 224"
                                                                                                                                                                                                                                                                                                                                              /note= "Represents FimH residue 226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pallesen L,
                                                                                                                                                                                                                                                  "..4
'note= "Linker peptide"
                                                                                                                                                                                                                                                                                                   20..22
/note= "Linker peptide"
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 58; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molin S,
                                                                                                                                                                      Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-DK00042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0187166
                                                                                                                                                         Chimeric - Vibrio cholerae
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GXBI-) GX BIOSYSTEMS AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hasty DL, Klemm P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-275442/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and microbial celthe adhesins bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ93061
                                                                                                                                                                                                    Key
Misc-difference
                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                         WO9520657-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1995;
                                                       18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1995
                            AAR76748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                     Peptide
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Rivaille P, Siffert O, Dodin A;

82FR-0009167. 83EP-0401052.

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The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP910264, AAP910600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                         Length 26;
                                                                                                                                                                                                                                                                                                                                                            Score 62; DB 4; Length 26 Pred. No. 7.4e-05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP50439 standard; protein; 41 AA.
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0
                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 AA;
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50439;
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Gaps

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Indels

Length 23;

Query Match 100.0%; Score 62; DB 16; Best Local Similarity 100.0%; Pred. No. 6.5e-05; Matches 12; Conservative 0; Mismatches 0;

1 VEVPGSQHIDSQ 12

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The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AA230264, AA230265, AA200600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                                                                               interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of amino acids 350-75 of the cholera toxin B1 subunit which carries an Arg at posns. 35, 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                               ;
0
New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholera vaccine; therapy; E.coli infection; enterotoxin LT
                                                                                                                                                                                                                                                                                                          Length 46;
                                                                                            The repeating units are bonded together by intramolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodin A;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                      100.0%; Score 62; DB 6; 100.0%; Pred. No. 0.00014; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siffert 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rivaille P,
                                                      Claim 8; Page 100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP30600 standard; Protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Page 11; 13pp; French.
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PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a vaccine 1-10mg of active cpd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82FR-0009167.
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.000
These 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milhaud G, Raulais D, I
Guyongruaz A, Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                     27
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                                                                                                                                                                                                                                                                                                                                                                                                         16 vevpgsghidsg
                                                                                                                                                                                                                                                                                                                                                                                     1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                  46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CNRS ) CNRS (INSP ) INST
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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP30600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                                                                                                                                                                                                             New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
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100.0%; Score 62; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels
                Heat-labile enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat-labile enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                     8; Page 100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP50436 standard; protein; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84WO-US02030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83US-0559469
                                                                                                                                                                     84WO-US02030
                                                                                                                                                                                                         83US-0559469
                                                                                                                                                                                                                                              (SCRI-) SCRIPPS CLINIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1985-159230/26.
                                                                                                                                                                                                                                                                                                                         WPI; 1985-159230/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AA;
                                                                                                                                                                   12-DEC-1984;
                                                                                                                                                                                                         12-DEC-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghten RA;
                                                                                                                                                                                                                                                                                      Houghten RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO8502611-A
                                                                                        WO8502611-A
                                                                                                                               20-JUN-1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                                                                                                New method for producing modified pertussis holotoxin
                                                                          Escherichia coli verotoxin-1 B-subunit.
AAY41816
ID AAY41816 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                              Cockle SA,
                                                                                                                                                                                                                  94US-0292968.
93US-0110947.
94US-0251121.
                                                                                                                                                                                              95US-0467974.
                                                     (first entry)
                                                                                                                                                                                                                                                             (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                              Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                             WPI; 1999-579908/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                ADP-ribosylating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 AA;
                                                                                                                                                                                              06-JUN-1995;
                                                     08-DEC-1999
                                                                                                                                                                                                                              24-AUG-1993;
31-MAY-1994;
                                                                                                                                Escherichia
                                                                                                                                                    US5965385-A
                                                                                                                                                                        12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention
                                AAY41816;
                                                                                                                                                                                                                                                                                             Read RJ,
                                                                                                                                                                                                                                                                                                         Hazes B,
             ó
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes with
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 93;
                                Length 47;
                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 62; DB 16; Length 9
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coll heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                              Score 62; DB 4; I
Pred. No. 0.00014;
                                                                                                                                                                                                                  ADP-ribosylating toxin (verotoxin-1 B-subunit).
                                                    Mismatches
                                                                                                                                                 AAR72545 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 54pp; English.
                                                     ;
0
                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Armstrong GD, Cockle SA, Ha
Oomen R, Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                      93US-0110947.
94US-0251121.
                                                                                                                                                                                                                                                                                                                                                   94EP-0306219
                                                                                                                                                                                                                                                                                                                                                                                                      (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                              (first entry)
                              Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                         1 VEVPGSQHIDSQ 12
                                                                                      WPI; 1995-132623/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pertussis infection
  ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other molecules
 47
                                                                                                                                                                                                                                                                                                                                                 23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                              28-NOV-1995
                                                                                                                                                                                                                                                                                  Bacteria sp.
                                                                                                                                                                                                                                                                                                                             05-APR-1995,
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                                                                                                                                                                       AAR72545;
 Sequence
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Klein MH,

Loosmore S,

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Involving analysis of the 3-dimensional form of the crystalline involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertursis holotoxin modification process comprises:

holotoxin for modification by analysing the 3-dimensional form of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structures of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect biological properties of the pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin the broad in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 62; DB 20; 100.0%; Pred. No. 0.0003;
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AAW95226
ID AAW9523
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Gaps

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1 VEVPGSQHIDSQ 12

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RESULT

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The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification.

The complexed with a polysaccharide molecule capable of forming a complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAY68340 to AAY68385 represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor; islet-activating protein.
                                       Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crystalline form of isolated pertussis holotoxin useful in studying proteins which have functional resemblance -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 21; L
Pred. No. 0.0003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cockle SA, Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E coli verotoxin-1 B subunit SEQ ID NO: 26.
Heat labile toxin B subunit SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB66239 standard; Protein; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 5; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                              95US-0467976.
                                                                                                                                                                                                                                                                                                                        94US-0292968
                                                                                                                                                                                                                                                                                                                                            93US-0110947
94US-0251121
                                                                                                                                                                                                                                                                                                                                                                                                        (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.

Best Local Similarity 100.

Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stein PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-136703/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VEVPGSQHIDSQ
                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                        22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                              24 - AUG - 1993;
                                                                                                           immunogenic.
                                                                                                                                                                                           US6018022-A.
                                                                                                                                                                                                                                     25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB66239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Read RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to methods of preparing a pertussis holotoxin (PT) having a modified biological activity. One method comprises identifying at least 1 site in a PT that interacts with a molecule that is capable of forming a complex with the holotoxin and which molecule is an effector molecule which is an adenine nucleotide and which site contributes to toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional structure of crystalline PT, determined by X-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure of crystalland and or structural resemblance to other bacterial toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
                                                                                                                    Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 20; Length 93; Pred. No. 0.0003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loosmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                               E. coli heat-labile toxin (LT) beta-subunit sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iD, Cockle SA, Hazes B,
Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 5; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                        94US-0292968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY68365 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0110947
94US-0251121
                                                                                                                                                                                                                                                                                                                                                           94US-0292968
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                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-105104/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA;
                                                                                                                                                                                      heat-labile; LT
                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Armstrong GD,
                                                                                                                                                                                                                                                                                                                                                              22-AUG-1994;
                                       16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2000
                                                                                                                                                                                                                                                                          US5856122-A
                                                                                                                                                                                                                                                                                                                    05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY68365;
AAW95226;
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Klein MH, Armstrong GD;

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Gaps

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14

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AAY68365 RESULT

0 x 2 x 5 x

Length 93; Indels

Escherichia coli.

US6168928-B1

02-JAN-2001

Oomen RP,

Cockle SA,

Stein PE;

Read RJ, Hazes B,

WPI; 2001-122260/13.

(CONN-) CONNAUGHT LAB LTD.

94US-0292968. 93US-0110947. 94US-0251121.

24-AUG-1993; 31-MAY-1994;

98US-0082514.

21-MAY-1998; 22-AUG-1994; Example 3; Fig 5; 41pp; English.

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The inventors claim vaccines against cholera and heat-labile E.coli toxin contg. cholera toxin fragment coupled to carrier. The toxin is esp. the fragments defined in FT, above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin; structural protein; receptor; heterologous gene; leader; promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant constructs comprising a promoter functional in Bordetella operatively linked to a heterologous gene or a non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella pertussis; whooping cough; recombinant construct;
                                                                                                                                                                                                                                                                                                                                                                                             Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                   Vaccines against cholera and heat-labile E. coli toxin cholera toxin fragment coupled to carrier
                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 6; I
Pred. No. 0.00034;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loosmore SM, Yacoob RK, Zealey GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW04857 standard; Protein; 103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Figure 1; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic cholera toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                 (YEDA ) YEDA RES & DEV CO LID.
                                                                                                                                                                                                                                        Example; Fig 1; 24pp; German
                                               83IL-0069558.
                                                                                                                  Sela M, Arnon R, Jacob CO;
            84DE-3430894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-CA00107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-425088/42.
N-PSDB; AAT38038.
                                                                                                                                                    WPI; 1985-069683/12
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                              103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qene of interest
            22-AUG-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1996;
                                             23-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9626282-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein MH,
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW04857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 17
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                        Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, call binding or enzyme activity of PT and modifying identified site
                                                                                                                                                                                                                                        Klein MH, Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 62; DB 22;
100.0%; Pred. No. 0.0003;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                          Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; cholera; heat-labile E.coli toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of sub-unit B of cholera toxin.
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AAP50340 standard; protein; 103 AA.

RESULT 16 AAP50340

Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative

93 AA;

Seguence

1 VEVPGSQHIDSQ 12

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5

40 vevpgsqhidsq

(first entry)

01-DEC-1991

AAP50340;

Location/Qualifiers

Vibrio cholera

50..64 /note= "claimed"

Region Region Region

Key

8..20 /note= "claimed" 45..64 /note= "claimed"

DE3430894-A. 14-MAR-1985.

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Gaps

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AAW06606
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Bordetella leader sequence for secretion of a gene product which may not be of Bordetella origin, can be used for the expression in Bordetella of enzymes, antigens, immunogens, allergens, enzyme inhibitors, hormones, immunoglobulins or their fragments, toxins, mammallan proteins, structural proteins or their receptors. The Bordetella strains are particularly engineered to express the cholera toxin a subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, that promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the pertussis toxin subunit sleader (S1-L), the pertussis toxin subunit sleader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a novel synthetic cholera toxin B gene (ctb) and the hmwl and hmw2
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit; vaccine; transgenic plant; immunogen; antigen;
                                                                                                                                                                                                                                                       100.0%; Score 62; DB 17; Length 103; 100.0%; Pred. No. 0:00034;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat labile enterotoxin B subunit (LT-B) E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mason HS;
                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 100-101; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clements JD, Hag TA,
                                                                                                                                                                                                                                                                                                                                                                                                  AAR94939 standard; Protein; 103 AA.
                                                                                                                                                                                      genes of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TULA ) TULANE EDUCATIONAL FUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TEXA ) UNIV TEXAS A & M SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US13376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-230602/23.
N-PSDB; AAT18799, AAT18800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adjuvant; immunisation
                                                                                                                                                                                                                                                                                                          1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                  Local Similarity
les 12; Conserv
                                                                                                                                                                                                                                                                                                                         103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9612801-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arntzen CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-1996
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR94939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxin;
                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to
plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or optionally LT-A or CT-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                       Length 103;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replaced by Asn'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- substitution
/note= "wild-type Ala replaced by
                                                                                                                                                       100.0%; Score 62; DB 17; 100.0%; Pred. No. 0.00034;
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic Escherichia Coli
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= substitution
/note= "wild-type Thr
Misc-difference 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= substitution
/note= "wild-type His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW06606 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Page -; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95SE-0001682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-SE00570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                               Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holmgren J, Lebens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                              1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT43576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                              103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9634893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06606;
                                                                                 Sequence
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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04-APR-1997;
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                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                       AAW80808;
                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                               AAW80808
                                                                                                                                                                                                                                                                                                                RESULT
    888888888888
                                                                                                                                                                                                                                            δ
                                                                                                                                                                                    ö
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to
              comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                  Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..25
/label- substitution
/note- "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
                                                                                                                                                                                    ö
protect against enterotoxigenic illness. Immunogenic proteins
                                                                                                                                                         100.0%; Score 62; DB 17; Length 103; 100.0%; Pred, No. 0.00034;
                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic Escherichia Coli.
                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                             AAW06607 standard; Protein; 103 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page -; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-SE00570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95SE-0001682.
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vomiting; food poisoning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmgren J, Lebens MR;
                                                                                                                                                                                                             1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                              WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HOLM/) HOLMGREN J.
(LEBE/) LEBENS M R.
                                                                                                                103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT43577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9634893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                      06-AUG-1997
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                                                                                     AAW06605).
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                          AAW06607;
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This is the amino acid sequence of the cholera toxin B subunit used in the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an entigen to birds and animals. In addition to the use of the toxin as an mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it enables the possibility for commercial mucosal adjuvants for use in humans, since these are more effective and safer than vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholera toxin B subunit, nontoxic subunit, adjuvant, coadministration, antigen; bird, animal; mucosal, vaccine.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered with an antigen to birds and mammals
                                      ដ
immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals. Note - This sequence does not appear in the specification, it is Note - This sequence of mature cholera toxin B subunit (see AAW06605).
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                           Length 103;
                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                         Score 62; DB 17;
Pred. No. 0.00034;
                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takeda Y, Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW80808 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1B; 43pp; English.
                                                                                                                                                                                                                                                         100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US06725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         administered subcutaneously
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.uv
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIYO/) KIYONO H.
(MCGH/) MCGHEE J R.
(TAKE/) TAKEDA Y.
(UABR-) UAB RES FOUND.
(YAMA/) :YAMAMOTO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kiyono H, Mcghee JR,
                                                                                                                                                                                                                                                                                                                                    1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                     50 vevpgsqhidsq 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-594478/50.
                                                                                                                                                                                                     103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
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103 AA;

Seguence

AAR04163

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us-09-786-648-3.rag

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protein with an epitope of a malaria parasite, eg Region I or Region II or a repeat region of circumsporozoite protein antigen (CS) (AAP93560) from Plasmodium berghei. Pref. the fusion gene is inserted into attenuated Salmonella enteriditis under the left promoter control of lambda. Such bacteria can multiply in the host without causing disease (disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be ultivalent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cholera toxin B subunit, used for hybrid immunogenic toxin production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patent, the DNA encoding LT-B is expressed as part of a fusion
                                                          subunit of the heat-labile enterotoxin (LT-B) derived from E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat labile, tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation;
                                                                                    B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malari.
circumsporozoite protein; fusion protein; live recombinant vaccine;
Salmonella; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising attenuated entero-invasive bacterium contg. \ensuremath{\mathsf{DNA}} encoding epitope of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
0.00041;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                              Hockmeyer WT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 62; 100.0%; Pred. No.
                                                                                                                                                                                                  1..22
/note="Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Live recombinant vaccine for malaria
                                                                                                                                                                                                                             23..124
/note="Mature LT-B"
                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              Pillai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                    88WO-US03376.
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                                                                                                                                                                                                                                                                                                                                                                                               (PRAX-) PRAXIS BIOLOGICS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.v.
The 12; Conservative
                            06-JUN-1990 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Majarian WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-114399/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAN90747.
                                                                                                                                                  Escherichía colí.
                                                                                                                                                                                                                                                                                                                                    30-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1987;
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                                                                                                                                                                                                                                                                                                      06-APR-1989
AAP93561;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Brey RN,
                                                                                                                                                                                                                             Protein
                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                     cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hybrid protein, useful in vaccines \mbox{-} contains cholera toxin b subunit and heterologous IgA active
                              Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 118;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              1..11
/*label= signal peptide
/*note= absent from mature protein
                            DB 19;
0.00034;
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 62; DB 11; Best Local Similarity 100.0%; Pred. No. 0.00039; Matches 12; Conservative 0; Mismatches 0;
                         Ouery Match
100.0%; Score 62; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYLI-) L'UNIVERSITE DE L'ETAT A LIEGE.
                                                                                                                                                                                                                                                                                                                                                                                         18..18
/*label= His or Tyr
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP93561 standard; protein; 124 AA.
                                                                                                                                                                                           AAR04163 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89WO-0000495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88FR-0012627
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; ; pp; French.
                                                                                                                                                                                                                                                                                      Cholera Toxin B-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VEVPGSQHIDSQ 12
                                                                                       1 VEVPGSQHIDSQ 12
                                                                                                                    50 vevpgsghidsg 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-132273/17
N-NSDB; Q04046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigenic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA;
                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1988;
                                                                                                                                                                                                                                                        10-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9003437-A
                                                                                                                                                                                                                                                                                                                                                synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L'Hoir C,
                                                                                                                                                                                                                           AAR04163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                              region
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Gaps

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Indels

RESULT 2 AAP93561 ID AAP9 XX

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96US-0747410 97WO-US20584

Ireland J;

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(UNMS ) UNIV MICHIGAN STATE.
                                                                                                                                                WPI; 1998-297947/26.
                                                                                                                                                           N-PSDB; AAV41573
                                                                                                                          Bagdasarian M,
               W09821344-A1
                                                         12-NOV-1997;
                                                                               L2-NOV-1996;
                                    22-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                  AAW06605 is the full (including the signal peptide) length cholera toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amino acids (aa) of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see AAW06605 and AAW06607. The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                     Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
immunogen; antigen; broad spectrum; cross reactive; diarrhoea;
vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 62; DB 17; Length 124; 100.0%; Pred. No. 0.00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                      1..21
/label= sig_peptide
                                                                                          22..124
/label- mat_protein
                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW59770 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of E. coli LTB.
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 32pp; English.
                                                                                                                                                                      96WO-SE00570.
                                                                                                                                                                                            95SE-0001682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                 Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                   WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AA;
                                                                                                                                                                                                                                                                                N-PSDB; AAT43575
                                  Vibrio cholerae.
                                                                                                                                                                                           05-MAY-1995;
                                                                                                                                                                      02-MAY-1996;
                                                                                                                          WO9634893-A1
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                                                                                                                                                07-NOV-1996
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                                                                    Peptide
                                                                                          Protein
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AAW59770
                                                          Key
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Beta-subunit of heat labile enterotoxin; LTB; fusion protein; vaccine; immunogen; antigen; inhibin; fertility; follicle stimulating hormone; FSH; sperm; ova; immune response.

Escherichia coli.

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                                                                                                                                                                                                                               This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (ITB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antiquence peptide is an inhibiton fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducting an immune response against the antigenic peptide. Vaccines are particularly administered orally, e.g. fusion protein is expressed in edible plants or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
New nucleic acid encoding fusion of antigenic peptide and enterotoxin sub-unit - useful as vaccinating immunogen, particularly for increasing animal fertility by inducing antibodies against inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 124;
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                                                                                                                                                                            Disclosure; Fig 9; 56pp; English.
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AA;
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3, Appli 4, Appli 4, Appli 4, Appli 3, Appli 3, Appli 14, Appli

Sequence Seq

Sequence 14, Sequence 20,

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

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APPLICANT: STEIN, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKIE, Stephen A.
APPLICANT: COCKIE, Stephen A.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
CORRESPONDENE ADDRESS:
ADDRESSEE: SIM & MCBULDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
US-09-039-609-2
US-08-416-950-11
US-07-672-304-3
US-07-672-304-3
US-08-011-398B-4
US-08-61-4
US-08-62-498-4
US-08-654-385-3
US-08-61-114
US-08-61-114
US-08-61-25-3
US-08-61-25-14
US-08-950-4421-14
US-08-950-4448-14
US-08-950-4448-14
US-08-950-4448-14
US-08-956-96-12
US-08-950-448-14
US-08-956-96-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-AMX-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1038-388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/08292968 Patent No. 5856122 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEWART, Michael I. REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 93 amino acids
IYPE: amino acid
    single
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STATE: Ontario
COUNTRY: Canada
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STRANDEDNESS:
TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-292-968-26
         Sequence 26, Appl
Sequence 26, Appl
Sequence 5, Appli
Sequence 6, Appli
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Sequence 17, Appli
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Sequence 2, Appli
Patent No. 5194375
Sequence 1, Appli
Sequence 4, Appli
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7.978 Million cell updates/sec
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Sequence 2, P
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Sequence 26,
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                                                                                                                                                                   July 16, 2001, 16:36:18; Search time 30.3 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-467-536-26
US-08-467-976-26
US-08-467-976-26
US-08-952-337-6
US-08-952-337-6
US-08-472-171-2
US-08-472-171-2
US-09-374-597-2
US-09-374-597-2
US-09-374-597-2
US-09-374-597-2
US-08-952-337-1
US-08-952-337-1
US-08-829-026A-6
US-08-449-045C-4
US-08-449-045C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-602-359A-34
US-08-878-989-2
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US-09-039-609-4
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US-09-027-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                               193259 seqs, 20144635 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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                                                                                                                       OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
                                                                                                                                                                                                                                                         US-09-786-648-3
62
1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,536
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-AMY-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-AMY-1994
PRIOR APPLICATION NUMBER: US 08/210,947
FILING DATE: 24-AUG-1993
ATTONENEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 2; 100.0%; Pred. No. 0.00027; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REPEROE_COCKET NUMBER: 1038-455 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite 701, 330 University
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
2IP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TO SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               Sequence 26, Application US/08467536 Patent No. 5977304
                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOCSMORE, Sheena
APPLICANT: LOCSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
ITLE OF INVENTION: WODIFICATION
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                         1 VEVPGSQHIDSQ 12
                                                   40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 VEVPGSQHIDSQ 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                     RESULT 3
US-08-467-536-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-467-536-26
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US-08-467-976-26
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0
                                                                   Length 93;
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                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STEIN, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOOSWORE, Sheena
APPLICANT: LOOSWORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
                                                                 Score 62; DB 2; I Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,993
REFERENCE/DOORET NUMBER: 1038-454 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-UN-1995
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/292,968
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08467974
Patent No. 5965385
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                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26
                                                               Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                        1 VEVPGSQHIDSQ 12
                                                                                                                                                                               40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                          RESULT 2
US-08-467-974-26
US-08-292-968-26
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Gaps

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Length 93; Indels

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Sequence 5, Application US/08952337
Patent No. 6019973
GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
ITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
ITLE PALLIER APPLICATION NUMBER: US/08/952,337
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1995-05-05
HUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 62; DB 4; Length 93; 100.0%; Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                   STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/082,514
FILLING DATE:
                                                   TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS:
                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STERRAT IN GIAGA! I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
     ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Vibrio cholerae
US-08-952-337-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-08-952-337-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                         MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORREL AFFILIATION NUMBER: US/08/467,976
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-A0C-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/21,121
FILING DATE: 31-MAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-A0C-1933
APPLICATION NUMBER: US 08/110,947
RIGHT STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-453 MI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/09082514
Patent No. 6168928
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: OOKCLE, Stephen A.
APPLICANT: OOMEN, RAYMOND P.
Sequence 26, Application US/08467976
Patent No. 6018022
                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite 701, 330 Univer:
CITY: Toronto
STATE: Ontario
COUNTR: Canada
ZIP: MSG 187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOSFWANE: PatentIn Release #1
                                                                    APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COSMORE, Sheena
APPLICANT: LOCSMORE, Sheena
APPLICANT: HOSMORE, Sheena
APPLICANT: HAZES, Bart
APPLICANT: HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-082-514-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Gaps

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APPLICANT: Loosmore, Sheena M
APPLICANT: Yacoob, Reza K
APPLICANT: Zealey, Gavin R
APPLICANT: Zealey, Gavin R
APPLICANT: Alein, Michel H
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
TUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6th Floor, ...
STREET: Ontario
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDPPy disk
COMPUTER: PRE-COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/894,526
FTLING DATE: 01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62; DB 2;
Pred. No. 0.0003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB 2;
Pred. No. 0.0003;
                                                                                                               1038-507 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               £: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
FILING DATE: 23-FEB-135-
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELEPONNICATION INFORMATION:
TELEPHONE: 416-595-1163
TELEEX: 065-2467 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-894-526-2
Sequence 2, Application US/08894526
Patent No. 5942418
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-472-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 VEVPGSQHIDSQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Consider, Sheena M.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Elin, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
SIN & McBurney
STREET: 330 University Avenue, Suite 701
CITY: Toronto
                                                                        ;
0
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REPERENCE: 3846/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT PILING DATE: 1998-01-05
EARLIER FILING DATE: 1996-01-05
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1996-05-05
SARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTERD for Windows Version 3.0
SEQ ID 0.05
                       Score 62; DB 3; Length 102;
Pred. No. 0.0003;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 102;
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100.0%; Pred. No. 0.0003;
ive 0; Mismatches 0; Indels
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STATE: Ontario
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                    Sequence 6, Application US/08952337
Patent No. 6019973
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Patent No. 5932714
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0
                       100.0%;
100.0%;
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US-08-952-337-6
                    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                         49 VEVPGSQHIDSQ 60
                                                                                                               1 VEVPGSQHIDSQ 12
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US-08-952-337-6
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TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
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Patent No. 6194560
GENERAL INFORMATION:
APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Hag
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/374,597
                                                                                                                                                 NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100 CITX: Houston STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1038-964
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/393,334
FILING DATE: FEBRUARY 23, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 416-595-1153
TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
      APPLICANT: Yacoob, Reza K. APPLICANT: Zealey, Gavin R. APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 103 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-374-597-2
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COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                  Toronto
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GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: Vaccob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Xealey, Gavin R.
APPLICANT: Staley, Gavin R.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains of Bordetella
STREET: 330 University Avenue, 6th Floor
STREET: Gontario
COUNTRY: Canada
ZIP: MSG IR7
COMMITTED
COMM
         Gaps
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         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,047
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100.0%; Pred. No. 0.0003;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE-POCKET NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 07-UN-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6140082
GENERAL INFORMATION:
APPLICANT: LOSEMORE, Sheena M.
                                                                                                                                                                                                                                            US-09-013-047-2
; Sequence 2, Application US/09013047
; Patent No. 5998168
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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; TOPOLGGY: linear
; MOLECULE TYPE: protein
US-09-013-047-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
      Conservative
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                                                                                                 50 VEVPGSQHIDSQ 61
12;
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      Matches
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Gaps

Length 103;

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100.0%; Score 62; DB 5; Length 10
100.0%; Pred. No. 0.0003; Nismafrhes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Eschcerichia coli
US-08-952-337-2
                                                                  Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Vibrio cholerae US-08-952-337-1
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                               1 VEVPGSQHIDSQ 12
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                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 62; DB 4; Length 103; 100.0%; Pred. No. 0.0003; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Houston
STARE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W.
REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36170/3P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 P01590US1
APPLICATION NUMBER: US/09/191,852 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-13376-21; Sequence 21, Application PC/TUS9513376; GENERAL INFORMATION:
                                                                                                                                                                               REGISTRATION NUMBER: 40,612
REGISTRATION NUMBER: 40,612
REGERENCE/FOOCKET UNMBER: P01
TELECOMMUNICATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                       TELEPHONE: 713-651-5151
TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear us-09-191-852-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VEVPGSQHIDSQ 12
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PCT-US95-13376-21
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Matches 12; Conserv
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CITY: Houston
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Sequence 2, Application US/08952337

Batent No. 6019973

GENERAL INFORMATION:
APPLICANT: HOLMOTEN, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: BYENDED MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENFORMENT SOLOSY
CURRENT FILING DATE: 1998-01-05
EARLIER PILICATION NUMBER: US/08/952,337

CURRENT FILING DATE: 1996-05-02

EARLIER PLICATION NUMBER: SE 9501682-0

EARLIER FILING DATE: 1996-05-02

EARLIER FILING DATE: 1995-05-05

SOFTWARE: PRACE OF WINDOWS Version 3.0

SOFTWARE: PASTSEQ for Windows Version 3.0

SED ID NO. 2
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LODGE, Jan
APPLICANT: LODGES, Michael R.
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D78
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT PILING DATE: 1998-01-05
EARLIER PILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1996-05-05
SARLIER PILING DATE: 1996-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASELED for Windows Version 3.0
SEQ ID NO
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Matches 12; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
US-08-449-045C-4
Sequence 4, Application US/08449045C
Patent No. 5770203
GENERAL INFORMATION:
APPLICANT: Burnette, Neal W.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,026A
FILSSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0106.97
FELEPHONE: 301-504-5076
TELEPHONE: 301-504-5060
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Janelle S. Graeter
STREET: Room 411, Building 005, BARC-W
CITY: Beltsville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAY-1991
PRIOR APPLICATION NUMBER: US 08/271,222
APPLICATION NUMBER: US 08/271,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/449,045C
24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VEVPGSQHIDSQ 12
                                                                                                                                       USA
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                                                                                                                                       COUNTRY:
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APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                     Sequence 2, Application US/08747410

Patent No. 5993820

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
TITLE OF INVENTION: CHIMERIC LTB VACCINES
TORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 5993820west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ILP: 55402
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: DAISWette
COMPUTER: IBM Compatible
COMPUTER: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFCATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11526.1-US-01
TELEPHONE: 612/311-5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,410
FILING DATE: 12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-829-026A-6
; Sequence 6, Application US/08829026A
; Patent No. 5837825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 124 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VEVPGSQHIDSQ 12
                                                70 VEVPGSQHIDSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VEVPGSQHIDSQ 12
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ORIGINAL SOURCE:
US-08-747-410-2
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                 PARENT NO. 5223610
PAPPLICANT: BUTTON, Frank H.:Sutcliffe, Gregor
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                     Score 56; DB 6; Length 124;
Pred. No. 0.0044;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 EXECUTIVE SQUARE, STE 1400
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359
FILING DATE: February 16, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-602-359A-34; Sequence 34, Application US/08602359A; Patent No. 5942430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MURPHY, Dennis

MURPHY, Dennis

REID, John
MAFFIA, Anthony
LINK, Steven
SWANSON, RODAIG V.
WARREN, PALLICK V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAK: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 34:
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Best Local Similarity 91.7%;
Matches 11; Conservative
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LENGTH: 346 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-602-359A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: LA JOLLA
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                                , LENGTH: 124
5223610-3
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-08-435-605A-12

Sequence 12, Application US/08435605A

Patent No. 5874287

GENERAL INFORMATION:

APPLICANT: Burnette, W. Neal

APPLICANT: Raslow, Harvey R.

TITLE OF INVENTION: SUBUNIT ANALOGS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 De Havilland Drive

CITY: Thousand Oaks

STATE: California
                                                                                                                                                                                                                                                                                       Query Match 90.3%; Score 56; DB 1; Length 124; Best Local Similarity 91.7%; Pred. No. 0.0044; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.3%; Score 56; DB 2; Length 124; 91.7%; Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NORMER: US/08/435,605A
FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                        NAME: Mazza, Richard J.
REGISTATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: 4-19
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mazza, Richard J.
REGISSRATION UNDABER: 27,657
REFERENCE CDOCKET NUMBER: A-19
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 maino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
FILING DATE: 06-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-435-605A-12
                                                                                                                                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
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71 VEVPSSQHIDSQ 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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RESULT

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APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TANG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,3378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                    GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Corley, Nail C.
APPLICANT: Corley, Nail C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guejler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
ITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSeg for Windows Version 2.0
SUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 4
Pred. No. 44;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09027337B Patent No. 5972616 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                    Sequence 2, Application US/09272796 Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.7
Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CLONE: 40194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                     Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE
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US-09-027-337-2
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Score 39; DB 2; Length 346;
Pred. No. 15;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Glegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 2;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATE: APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0321 US
TELECOMNUNICATION:
TELEPHONE: 415-655-0555
                                                                                                                                                                                                            Sequence 2, Application US/08878989
Patent No. 5885803
62.9%;
54.5%;
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3,
                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: TBLYNOT01; CLONE: 40194
US-08-878-989-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 VHTPNSQKVDSQ 285
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                                                                                                11111: 1:::
309 VEVPGAGHVEA 319
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                                                                            1 VEVPGSQHIDS 11
Query Match
Best Local Similarity
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                                                                                                                                                                      RESULT 22
US-08-878-989-2
                                      Matches
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CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 2

LENGTH: 855

TYPE: PRT

ORGANIZM: Homo sapiens

COTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides

OTHER INFORMATION: 23 to 2589 of Sequence 1

US-09-027-337-2
                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 25
5194375-6
; PALCANT: PARK, LINDA S.;GOODWIN, RAYMOND G.
; TITLE OF INVENTION: DNA ENCODING INTERLEUKIN-7 RECEPTORS AND
; METHOS OF USE
: NUMBER OF SQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,588
FILING DATE: 21-MAY -1990
; RPIOR APPLICATION DATA:
APPLICATION NUMBER: 421.201
; FILING DATE: 13-OCT-1989
; SEQ ID NO:6:
; LENGTH: 459
; LENGTH: 459
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                                                                                                                                                                                                                                            Score 36; DB 2; Length 855;
Pred. No. 1.4e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                            Query Match 58.1%;
Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 66.7'
Matches 6; Conservative
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370 IEVPNNQHV 378
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Search completed: July 16, 2001, 16:36:18 Job time: 207 sec

:|| ||||: 46 LEVDGSQHL 54

1 VEVPGSQHI 9

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

Run on:

July 16, 2001, 16:37:00; Search time 34.9 Seconds (without alignments) 26.192 Million cell updates/sec

US-09-786-648-3 62 Perfect score: Title:

1 VEVPGSQHIDSQ 12 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cholera enterotoxi	heat-labile entero	hypothetical prote	protein F20B17.2 [hypothetical prote	(S)-2-hydroxy-acid	hippocampus-derive	carbon-monoxide de	hypothetical prote	gibberellin 20-oxi	chorismate synthas	hypothetical prote	zuotin-like protei	hypothetical prote	probable 4-carboxy	glucarate dehydrat	probable membrane	cytochrome-c oxida	hydrolase BH3805 [methylenetetrahydr	catechol 1,2-dioxy	hypothetical prote			stress-activated p	hypothetical prote	monophenol monooxy	hypothetical prote	beta-fructofuranos
SUMMARIES																														
SUM	ΙD	XVVCB	OLECB	T34767	C96827	T14755	H75446	A35781	A41670	B85518	T01751	S17246	G96554	T39683	T01770	T47115	A69753	S 53976	S28757	E84125	F82031	JN0143	G83368	S23861	T29750	JC5694	T29029	S53529	T24379	T02092
	DB	П		~	7	7	7	7	Н	7	7	-	7	~	~	7	-	~	~	~	7	C\$	7	7	7	7	7	7	7	7
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	Query	100.0	100.0	64.5	62.9	65.9	62.9	61.3	61.3	59.7	59.7	59.7	59.7	59.7	59.7	58.1	58.1	58.1	56.5	56.5	56.5	56.5	56.5	9	ė	ė.	56.5	Ġ.		56.5
	Score	62	62	40	39	39	39	38	38	37	37	37	37	37	37	36	36	36	32	35	32	35	32	35	35	35	35	35	35	35
	Result No.		2	m	4	ស	9	7	œ	6	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

chitin synthase (E	faciogenital dyspl		hypothetical prote	hypothetical prote	hypothetical prote	NADH dehydrogenase	probable molybdenu	hypothetical prote	hypothetical prote	hypothetical prote	transcription regu	cell division prot	probable cell divi	conserved hypothet	hypothetical prote
A41638	A55380	T29041	G71611	T27563	T45990	T01091	B83584	T31648	G84353	T41734	C83388	G75126	A71005	H82640	T15846
~	7	7	7	7	7	~	7	7	7	C	7	7	~	~	7
096	961	1258	2206	168	181	244	252	269	274	285	295	365	365	378	398
56.5	56.5	56.5	56.5	54.8	54.8	54.8	54.8	54.8	54.8	54.8)	54.8	54.8	54.8	54.8	54.8
35	35	32	35	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

		olera enterotoxin, B chain precursor VC1456 [validated] - Vibrio cholerae (strain N	ta chain	
		, B chain precursor	Alternate names: enterotoxin beta chain	
SOLT 1	VCB	olera enterotoxin	Alternate names:	

Officient entercotani, B chalan precursor VIII-0 | Validated] - Vabrio cholerae (strain N officienate names: entercotani, B chalan precursor VIII-0 | Validate of Concerns of

A; Molecule type: DNA
A; Residues: 1-20, 'Q', '22-31, 'Q', '33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <SHI>
A; Residues: 1-20, 'Q', '22-31, 'Q', '33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <SHI>
A; Experimental source: classical biotype strain 569B
B; Dams, E.; de Wolf, M.; Dierick, W.; Dierick, M.; Di

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A; Molecule type: DNA
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 <R
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 <R
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 68
A; Reterences: GB: 860731; NID: 9408994; PIDN: AAC60441.1; PID: 9408996
R; Tsuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, .J.; Wada, K.;
Microb. Pathog. 2, 381-390, 1987
A; Ritle: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin 1
A; Reference number: A61475
A; Reference number: A61475
A; Reference number: A61475
A; Residues: 22-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-95, 'A', 97-122, 'E', 124 <TSU>A; Residues: 22-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-95, 'A', 97-122, 'E', 124 <TSU>A; Experimental source: Strain 240-3
C; Complex: the heat-labile enterotoxin molecule contains one A chain and five or six C; Function: the biological activity of the toxin is produced by the A chain, which C; Superfamily: cholera enterotoxin beta chain
C; Superfamily: cholera enterotoxin beta chain
C; Superfamily: enterotoxin
C; Superfamily: enterotoxin chain B #status predicted <MAT>C; B17/Domain: signal sequence #status predicted
E; 30-107/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                             R;Dallas, W.S.; Falkow, S.
Nature 288, 499-501. 1980
A;Title: Amino acid sequence homology between cholera toxin and Escherichia coll heat
A;Reference number: A01820; MUID:81074965
                                                                                                                                                                                                                                                                                                                                                                                                               R:Yamamoto, T.; Gojobri, T.; Yokota, T.
J. Bacteriol. 169, 1352-1357, 1987
A;Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichi
A;Reference number: A26946; MUID:87137303
A;Accession: B26946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Wolecule type: DNA
A;Residues: 1-5, F', 17, 17, 'C', 19-24, 'S', 26-27, 'E', 29-33,'H', 35-63,'K', 65-66,'A', 68-122
A;Crosx-references: GB:M/874; NID:9145830; PIDN:AAA98064.1; PID:9145831
A;Experimental source: plasmid ENT-R PGG86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ibrahimi, I.; Gentz, R.
J. Biol. Chem. 262, 10189-10194, 1987
A;Title: A functional interaction between the signal peptide and the translation appa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues; 1.27, E'.29-63, K',65-124 <XAM>
A; Cross-references: EMBL:MIS363; NID:g148335; PIDN:AAA24792.1; PID:g148336
R; Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect. Immun. 48, 73-77, 1985
A; Title: Nuclectide sequence comparison between heat-labile toxin B-subunit cistrons
A; Reference number: I41194; MUID:85156481
A; Reference number: I41194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
FEMS Microbiol. Lett. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic A;Reference number: 153542; MUID:93252225
                                                                                                                      C;Species: Escherichia coli
C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999
C;Accession: A01820; B26946; I41194; I41287; I67644; A61475
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                                                                                            heat-labile enterotoxin chain B precursor - Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; 1
0.00014;
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A;Molecule type: DNA
A;Residues: 1-22 <RE2>
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 141287; MUID:87280041
A; Accession: 141287
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Local Similarity 100.0%;
hes 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A01820
A; Molecule type: mRNA
A; Residues: 1-124 <DAL>
R; Yamamoto, T.; Gojobori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
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Matches
Almolecular type: DNA

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Matches 12; Conserv
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Gaps

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Indels

Mismatches

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1 VEVPGSQHIDSQ 12

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A, Accession: H75446
A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, CLOSS-I-353 - WHID
A, CLOSS-Ireferences: GB-AE001954; GB: AE000513; NID: 96458751; PIDN: AAF10604.1; PID: 9645
A, Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ernfors, P.; Ibanez, C.F.; Ebendal, T.; Olson, L.; Persson, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 5454-5458, 1990
A;Title: Molecular cloning and neurotrophic activities of a protein with structural s
A;Reference number: A35781; MUID:90319130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (S)-2-hydroxy-acid oxidase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accesion: H75446
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shan, M.; Yamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hippocampus-derived neurotrophic factor precursor - rat
N'Alternate names: neurotrophin-3 precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 16-Jul-1999
C;Accession: A35781; A40094
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                      R; Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, August 1999
A; Reference number: 218181
A; Accession: T14755
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-272 <WAM>
A; Residues: 1-272 <WAM>
A; Experimental source: fetal brain; clone DKFZp564A0122
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                        Length 272;
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2;
Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  62.9%;
66.7%;
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75.0%;
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A;Molecule type: mRNA
Residues: 1-282 <ERN>
A;Cross-references: GB:M34643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
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246 ELPGSEHIE 254
                                                                                                                                                                                                                                                                                           A; Note: DKFZp564A0122.1
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  C; Accession: T14755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Nature 408, 816-820, 2000
A: Hunter: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Athors: Salzberg, S.L.; Sakano, H.
A; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Mitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
                                                                                                                                                                          C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
R; Murphy. L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A; Recession: T34767
A; Stetus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-242 AMR>
A; Residues: 1-242 AMR>
A; Cross-references: EMBL:AL031184; PIDN:CAA20190.1; GSPDB:GN00070; SCOEDB:SC2A11.21C
C; Genetics:
A; Genetics: A; Genetics: Strain A3(2)
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A;Residues: 1-260 <STO>
A;Cross-references: GB:AE005173; NID:g7715588; PIDN:AAF68106.1; GSPDB:GN00141
C;Genetics:
A;Gene: F20B17.2
A;Map position: 1
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C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein F20817.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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4.7;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.5%;
70.0%;
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50.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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65 VKVPGKQHVSEK 76
71 VEVPGSQHIDSQ 82
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204 VEVPGTDHTD 213
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Best Local Similarity
Matches 6; Conserv
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R; Theologis, A.; Ec
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Length 352;

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DB 7

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Score 37;
Pred. No. 2
                      59.7%;
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87.58;
                                                              6; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                           320 VVVPGANHVD 329
                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                   1 VEVPGSQHID 10
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hypothetical protein 20347 [imported] - Escherichia coli (strain O157:H7)
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Bascharichia coli
C; Accession: B85518
R; Perna, N. T; Plunkett III, G;; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: B85518
A; Accession: B85518
A; Molecule type: DNA
A; Residues: 1-552 csro>
A; Molecule type: DNA
A; Residues: 1-552 csro>
A; Cross-references: GB:AE005174; NID:912513064; PIDN:AAG54606.1; GSPDB:GN00145; UWGP:203
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Genetics:
A; Genetics:
    Maisonpierre, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furth, M.E.; Lindsay, R.M.;
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R; Maisonpierre, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furth, M.E.; Science 277, 146-1451, 1990
A; Title: Neurotrophin-3: a neurotrophic factor related to NGF and BDNF. A; Reference number: 440094; MUID:90208301
A; A; Accession: A40094
A; A; Accession: A40094
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 25-282 AMA1
A; Cross-references: GB: M33968; NID:9205771; pIDN:AAA41727.1; PID:9205772
C; Superfamily: nerve growth factor beta chain
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                                                                                                                                                                                                                                         Length 282
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Pred. No. 13;
3; Mismatches
                                                                                                                                                                                                                                       61.3%;
54.5%;
                                                                                                                                                                                                                                                                           6; Conservative
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Best Local Similarity
.....hag 6; Conserve
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Best Local Similarity
Matches 6; Conserva
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| VDVPGNSHTDA 11
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Rymanka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M. submitted to the EMBL Data Library, July 1998
A; Description: Over-expression of a tobacco homeobox gene, NTH15, decreases the expression: T01751
A; Reference number: 214418
A; Accession: T01751
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-367 cTAN>
A; Cross-references: EMBL:AB016084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chorismate synthase (EC 4.6.1.4) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G2501; protein YGL148w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S17246; S64162
R;Jones, D.G.L.; Reusser, U.; Braus, G.H.
Mol. Microbiol. 5, 2143-2152, 1991
A;Title: Molecular cloning, characterization and analysis of the regulation of the AR A;Reference number: S17246; MUID:92114793
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A; Molecule type: DNA
Residues: 1.376 <VVOL>
A; Cross-references: EMBL:272670; NID:91322731; PIDN:CAA96860.1; PID:91322732; GSPDB:G
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                                                                                                                                                                                                                                                                               glaberellin 20-oxidase - common tobacco
N.Alternate names: Nco16 protein
C;Species: Nicotlana tabacum (common tobacco)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
C;Accession: T01751
   Gaps
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A; Residues: 1-376 <JONN
A; Residues: 1-376 <JONN
A; Ross-references: EMBL:X60190; NID:93386; PIDN:CAA42745.1; PID:93387
A; Cross-references: EMBL:X60190; NID:93386; PIDN:CAA42745.1; PID:93387
B; Volckaert, G: Voet, M.; Verhasselt, P.; Defoor, E.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64153
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C;Keywords: phosphorus-oxygen lyase; transmembrane protein
F;347-363/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Ntc16
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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   2; Mismatches
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A;Map position: 7L
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Pred. No. 3
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C; Genetics:
A; Gene: SGD:ARO2; MIPS:YGL148w
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probable 4-carboxymuconolactone decarboxylase / 3-oxoadipate enol-lactone hydrolase [
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R;Yang, K.; Iwagami, S.; Davies, J.E.
submitted to the EMBL Data Library, May 1999
A;Description: A protocatechuate catabolic gene cluster cloned from Streptomyces sp. A;Reference number: Z24354
A;Accession: T47115
                                                                                                                                                                                                                                                                          hypothetical protein A_IG002P16.9 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse ear cress) C.Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 22-Oct-1999 C.Accession: T01770 #sequence_revision 19-Feb-1999 #text_change 22-Oct-1999 C.Accession: T01770 To Table To The EMBL Data Library, June 1997 A.Description: The sequence of A. thaliana IG002P16.

A.Reference number: 214421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces sp.
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
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C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                      Gaps
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  Length 442;
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red. No. 44;
Mismatches 1
  Score 37; DB 2;
Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 2;
Pred. No. 44;
0; Mismatches
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A;Experimental source: strain 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Residues: 1-550 <MIL>
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  59.78;
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55.6%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
                                                      Conservative
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371 DVPSAEHVDS 380
Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                          2 EVPGSQHIDS 11
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A; Residues: 1-373 <YAN>
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225 VEIPGASHL 233
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                                                                                                                                                                                                                                                                                  Cipecies: Arabidopsis thaliang (mouse-ear recess)
Cipecies: Arabidopsis thaliang (mouse-ear recess)
Cipace: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipacession: G96554
RTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hungles, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, Y.; Lin, X.; Liu, X.; Liu, Z.A.; Liu, Z.A.; Liu, S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
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R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, March 1998
A; Reference number: 221869
A; Accession: T39683
A; Coros: Teference DNA
A; Residues: 1-124 <OLI>A; Molecule type: DNA
A; Residues: 1-124 <OLI>A; Molecule type: DNA
A; Residues: Strain 972h:; cosmid c1778
A; Experimental source: strain 972h:; cosmid c1778
B; Wood, V; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A. submitted to the EMBL Data Library, February 1998
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A;Experimental source: strain 972h-; cosmid c30D10
C;Genetics:
A;Genetics:
A;Gene: SPDB:SPBC1778.01c; SPDB:SPBC30D10.01
A;Hap position: 2
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C;Species: Schizosaccharomyces pombe
C;Spate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T39683; T40195
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                                                                                                                                                                                                                                                            hypothetical protein F19C24.16 [imported] - Arabidopsis thaliana
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A; Accession: T40195
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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Pred. No. 33;
1; Mismatches
  ed. No. 29;
Mismatches
70.0%; Pred. No.
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75.0%;
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
Thes 6; Conserve
                                                                                                                               264 VSVPGSKHND 273
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                                                                              1 VEVPGSQHID 10
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A;Molecule type: DNA
A;Residues: 1-423 <STO>
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403 VPGIQHVD 410
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A;Gene: F19C24.16
A;Map position: 1
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Length 1785;

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58.1%;
ilarity 54.5%;
Conservative
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                                                                                                                                                                                                                                                                                                        403 EWPGAQHLSSR 413
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135 VSVTGSEHLD 144
                                                          Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-259 <STO>
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Best Local Similarity
Matches 6; Conserv
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R; Takami, H.; Nakasc
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Cixcession A09/33
Cixcession A09/26, 1997
Cixcit A00/200
Cixcit A00/2
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Pred. No. 55;
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<TM14>
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75.0%;
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Matches 6; Conserv
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64 EVPGGEHI 71
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A; Genome: mitochondrion
A; Genetic code: SGC4
C; Superfamily: cytcohrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C; Keywords: copper; electron transfer; heme; magnesium; membrane-associated complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masul, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20263314
A;Accession: E84125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytochrome-c oxidase (EC 1.9.3.1) chain I - blue mussel mitochondrion (fragments) C; Species: mitochondrion Mytilus edulis (blue mussel) C; Date: 20-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 07-Dec-1999 C; Accession: S28757 Boore, J.L.; Brown, W.M. Genetics 131, 397-412, 1992 A; Flefrann, R.J.; Boore, J.L.; Brown, W.M. A; Flefrance number: S28743; MUID:92354892 A; Flefrance number: S28743; MUID:92354892 A; Molecule type: DNA A; Molecule type: Molecule type:
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A.Experimental source: strain C-125
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
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Score 36; DB 2; L. Pred. No. 2.5e+02; 3; Mismatches 2;
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Pred. No. 24;
2; Mismatches
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A;Cross-references: EMBL:M83761; EMBL:M83762
C;Genetics:
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Pred. No. 4
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Gaps

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Indels

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Pypothetical protein 2 - Pseudomonas aeruginosa
Dypothetical protein 2 - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C;Accession: 523861
R;Huang, H; Siehnel, R.J; Bellido, F; Rawling, E.; Hancock, R.E.W.
submitted to the EMBL Data Library, July 1992
A;Description: Analysis of two gene regions involved in the expression of the imipene
A;Reference number: 523859
                                                                               A; Residues; 1-1-367 <STO>
A; Cross-references: GB:AE004648; GB:AE004091; NID:g9948237; PIDN:AAG05606.1; GSPDB:GN
A; Experimental source: strain PAO1
C; Genetics:
A; Genetics:
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein B0218.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T29750
R;Woessner, J.; Wohldmann, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 50/2; 239/1; 360/3
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A). Cross-references: EMBL: Z14064; NID: 945366; PIDN: CAA78447.1; PID: 945369
                                                                                                                                                                                                                                                                                                                                               Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 67;
2; Mismatches
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Pred. No. 68;
2; Mismatches
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85.7%; Pred. No. 69;
iive 0; Mismatches
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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity
'...hes 5; Conserve
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Matches 6; Conserv
                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO>
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A;Molecule type: DNA
A;Residues: 1-371 <HUA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VPGSQHID 10
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A; Accession: G83368
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K.; Lim,
                                                                                                                                                       Ryparkhili, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel and Mature 404, 502-506, 2000

Mature 404, 502-506, 2000

Mature 404, 502-506, 2000

MyTitle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.

MyReference number: A81775; MUD: 20222556

MyAccession: R82031

MyAccession: R82031

MyRelaus: preliminary

MyMolecule type: DNA

MyRelaus: 1-284 < PAR.

MyRelaus: 1-284 < PAR.
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R; Kivisaar, M.; Kasak, L.; Nurk, A.
Gene 98, 15-20, 1991
A; Title: Sequence of the plasmid-encoded catechol 1,2-dioxygenase-expressing gene, pheb, A; Reference number: JN0143; MUID:91192610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Tile: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
                            methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / methenyltetrahydrofolate
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Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
CiAccession: G8336
Ristover, C.R.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas sp.
C;Date: 05-Mar_1993 #sequence_revision 05-Mar-1993 #text_change 29-Sep-1999
                                                                C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catechol 1,2-dioxygenase (EC 1.13.11.1) - Pseudomonas sp. plasmid EST1001
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C;Superfamily: catechol 1,2-dioxygenase
C;Keywords: aromatic hydrocarbon catabolism; oxidoreductase
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51;
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4; Mismatches
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A; Residues: 1-302 <KIV>
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stress activated protein kinase (EC 2.7....) JNKD - common carp
N.Alternate names: stress-activated protein kinase b
C.Species: Cyptinus carpio (common carp)
C.Species: Cyptinus carpio (common carp)
C.Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999
C.Accession: JC5694
R.Hashimoto, H.; Matsuo, Y.; Yokoyama, Y.; Toyohara, H.; Sakaguchi, M.
J. Blochem. 122, 381-386, 1997
A.Fille: Structure and expression of carp mitogen-activated protein kinases homologous t
A.Recession: JC5693; MUID:97456373
A.Accession: JC5694
A.Status: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-477
A.Accession: J-477
A.Accession: J-47
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Search completed: July 16, 2001, 16:37:01 Job time: 210 sec

4 PGSQHID 10 ||| ||| 226 PGSDHID 232

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SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Elles, Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEQUENCE FROM N.A.
STRAIN=EL TOR 2125;
MEDLINE=84068199; PubMed=6646234;
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
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STRAIN-1854 / 0139-BENGAL;
Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
                                                                                                                                                                                                                                                                                                                                                         Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-84061784; PubMed-6315707;
Lockman H., Kaper J.B.;
Luckman H., Kaper J.B.;
Vucleotide sequence analysis of the A2 and B subunits of Vibrio cholerae enterotoxin.;
J. Biol. Chem. 258:13722-13726(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-4260B / SEROTYPE 0139;
MEDLINE-94237453; Pubmed-8181723;
Lebens M., Holmgren J.;
Structure and arrangement of the cholera toxin genes in Vibrio cholerae 0139.";
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to the EMBL/GenBank/DDBJ databases.
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13-UUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
CTXB OR TOXB OR VC1456.
                                                                                                                                                                                   ALIGNMENTS
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                       FTSQ_STRCU
YAAN_BACSU
VNUC_THOGY
A37C_DROME
YOG1_CAEEL
HEM1_AGABI
PD14_MOUSE
MAK5_YEAST
DPOUL_HPBVR
MML7_MYCTU
MASP_RAT
MOB2_YEAST
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Nature 306:551-557(1983).
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STRAIN-EL TOR 2125;
Dams E., de Wolf M.,
Submitted (MAY-1991)
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Vibrio cholerae.
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Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  METITE E.A., SATATY S., JODING M.G., Chang T., Holmes R.K.,
Hirst T.R., Hol W.G.J.;
"Structural studies of receptor binding by cholera toxin mutants.";
Protein Sci. 6:1516-1528(1997).
-I- FUNCTION: THE BETA CHAIN AGGREGATE (B.SUBUNIT) IS INVOLVED IN
BINDING TO CELL MEMBRANES.
-I- SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN
(FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAIN
DISULEIDE BOND, ASSOCIATE NONCOVALENTY WITH AN AGGREGATE OF 4 TO
                                                                                                                                                                                                                                                                                                                                  7.
                                                                                                                                      SEQUENCE OF 22-124.
MEDLINE-78005536; PubMed-903362;
Lai C.-Y.,
"Determination of the primary structure of cholera toxin B subunit.";
J. Biol. Chem. 252:7249-7256(1977).
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Fraser C.M.;
                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-94272319; PubMed-8003954;
Merritt E.A., Sarfaty S., van den Akker F., L'Hoir C., Martial J.A.,
                                                                                                                                                                                                                                                            Crystal structure of cholera toxin B-pentamer bound to receptor GM
                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MDDLINE-93837394, Pubmed--568472,
Abang R.G., Westbrook M.L., Westbrook E.M., Scott D.L., Otwinowski
Maulik P.R., Reed R.A., Shipley G.G.;
The 2.4 A crystal structure of cholera toxin B subunit pentamer:
choleragenoid ";
J. Mol. Biol. 251:550-562(1995).
                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                   SEQUENCE OF 22-124.
MEDLINE-78005537; Pubmed-903363;
Kurosky A., Markel D.E., Peterson J.W.;
"Covalent structure of the beta chain of cholera enterotoxin.";
J. Biol. Chem. 252:7257-7264(1977).
                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
STRAIN-OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE-97376625; PubMed-9232653;
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EMBL; K01170; AAA27573.1; -.
EMBL; D30053; BAA06291.1; -.
EMBL; X58786; CAA41593.1; -.
EMBL; X76390; CAA5397.3.1; -.
EMBL; X76391; CAA5397.3.1; -.
EMBL; AE004224; AAF94613.1; -.
                                                                                                                                                                                                                                                                                 Protein Sci. 3:166-175(1994).
                                              Nature 406:477-483(2000).
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08-MAR-96.
23-DEC-96.
01-APR-97.
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PIR; A05130; A05130.
PIR; S14624; S14624.
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                                   cholerae
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Gaps
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MEDLINE-85156481; PubMed-3884513;
Leong J., Vinal A.C., Dallas W.S.;
Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coll of human and porcine origin.";
Infect. Immun. 48:73-77(1985).
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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01-JAN-1990 (Rel. 13, Last sequence update)
15-UUL-1999 (Rel. 18, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B, HUMAN) (LTH-B).
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                                                                             CHOLERA ENTEROTOXIN, BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 124;
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100.0%; Pred. No. 7.4e-05;
Memarches 0;
InterPro; IPR001835; -.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
Membrane; Enterotoxin; Signal; 3D-structure.
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STRAIN-ISOLATE H10407;
MEDLINE-83114628; PubMed-6759877;
                                                                                                                                                                                                                                                                                                                                                                                                                               13957 MW;
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Best Local Similarity 100.
Matches 12; Conservative
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                                                               1 VEVPGSQHIDSQ 12
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SEQUENCE FROM N.A.
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B, PORCINE) (LTP-B)
                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                        Escherichia coli
                                                                                                                                   NCBI_TaxID=562;
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                                 Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.; "Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of human strain
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99185101; PubMed=10085117; Matkovic-Calagovic D., Loregian A., D'Acunto M.R., Battistutta R., Tossi A., Palu G., Zanotti G.; "Crystal structure of the B subunit of escherichia coli heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxin carrying peptides with anti-herpes simplex virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 274:8764-8769(1999).
-!- FUNCITON: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY THE A CHAIN, WHICH ACTIVITES INTERCELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                            Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae."; Mol. Microbiol. 15:1165-1167(1995).
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H10407).
CRC64;
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STRAIN=ETEC LT 87;
Germani Y., Desperrier J.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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H -> Y (IN ISOLATE H
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Pred. No. 7.4e-05;
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                                                                                                         FEMS Microbiol. Lett. 108:157-161(1993).
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PRINTS; PR00772; ENTEROTOXINB
Enterotoxin; Signal; 3D-structure.
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                     MEDLINE=9325225; PubMed=8486242;
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EMBL; S60731; AAC60441.1; --
EMBL; X83966; CAA58800.1; --
PDB); ILTR; 23-WAR-99
INTERPIO; IPR001835; --
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Best Local Similarity 100.

Matches 12; Conservative
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STRAIN-ISOLATE H10407;
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                                                                                                                                                                                                                                                                                                                             MEDIATIVE—88156481; PubMed=3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit
cistrons from Escherichia coli of human and porcine origin.";
                                                                                                                                                     SEQUENCE FROM N.A.,
STRAIN=ISOLATE P307,
STRAIN=ISOLATE P307,
Dallas W.S., Falkow S.,
"Amino acid sequence homology between cholera toxin and Bscherichia coli heat-labile toxin.";
Nature 288:499-501(1980).
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MEDLINE-87137303; PubMed-3546273;
Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae 01.";
J. Bacteriol. 169:1352-1357(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-91238966; PubMed-2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R., "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).

**MEDLINE=92340541; PubMed-9478941.

Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.;

"Refined structure of Escherichia coli heat-labile enterotoxin,

close relative of cholera toxin.";

J. Mol. Biol. 230:890-918(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
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Nature 351:371-377(1991).
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                                                                                                                                                                                                                                                                                                                  STRAIN-ISOLATE P307;
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Gaps

124 AA.

PRT;

ELBP_ECOLI STANDARD; P32890; P13768; P01557; 21-JUL-1986 (Rel. 01, Created)

ELBP_ECOLI RESULT

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379 KIPGAYHIDYQ 389
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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ARO2 OR YGL148W.
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P28777;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: CATALYZES THE INTERCONVERSION OF CO AND CO2 AND THE SYNTHESIS OF ACETYL-COENZYME A FROM THE METHYLATED CORRINOID/IRON
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CARBON MONOXIDE DEHYDROGENERS SUBUNIT (EC 1.2.99.2) (CODH).
Moorella thermoacetica (Clostridium thermoaceticum).
Bacteria; Firmicutes; Bacillus/Clostridium group; Moorella group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92084676; PubMed-1748656;
Morton T.A., Runguist J.A., Ragsdale S.W., Shanmugasundaram T.,
Wood H.G., Ljungdahl L.G.;
                                                                                                                                                                                                HEAT-LABILE ENTEROTOXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                              100.0%; Score 62; DB 1; Length 124; 100.0%; Pred. No. 7.4e-05;
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SIGNAL 1 21
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                       EMBL; M17873; AAA98065.1; -. EMBL; M15363; AAA24792.1; -.
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                                                                1LTA; 31-JAN-94.
1LTB; 31-JAN-94.
1LTG; 15-SEP-95.
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31-JAN-94.
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B26946; QLECEB.
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124 AA;
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                                        M17101;
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P27989;
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MEDLINE-97197983; PubMed-9046099;
Woet M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert G.;
Voet M., Defoor E. an early unclonable 22.8 kb segment on the left arm
"The sequence of a nearly unclonable 22.8 kb segment on the left arm
"The sequence of a nearly unclonable 22.8 kb segment on the left arm
"The Saccharomyces cerevisiae reveals ARO2, RPL9A,
TIP1, MRPI genes and six new open reading frames.";
"Yeast 13:177-182(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-i- INDUCTION: BY AMINO ACID STARYATION.
-i- SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analysis of the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones D.G.L., Reusser U., Braus G.H.; "Molecular cloning, characterization and analysis of the regulation of the ARO2 gene, encoding chorismate synthase, of Saccharomyces cerevislae.";
SULFUR PROTEIN, CO, AND COENZYME A. CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: 5-0-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                        -!- COFACTOR: NICKEL ION.
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
-!- SIMILARITY: TO R.RUBRUM CARBON MONOXIDE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductas; Nickel; Iron-sulfur; Electron transport.
METAL 68 68 IRON-SULFUR (BY SIMILARITY).
METAL 71 71 IRON-SULFUR (BY SIMILARITY).
METAL 90 10 IRON-SULFUR (BY SIMILARITY).
SEOUENCE 674 Aa; 72924 MW; 54BA3D816C25F9FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Microbiol. 5:2143-2152(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHORISMATE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M62727; AAA23228.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: REDUCED FLAVIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 54...
6; Conservative
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3238486007698C2A CRC64;

50782 MW;

455 AA;

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SEQUENCE
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ST14_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
"Determination of a 21548 bp nucleotide sequence around the 24
degrees region of the Bacillus subtilis chromosome.";
Microbiology 141:269-275(1995).
-!- FUNCTION CATALYZES THE DEHYDRATION OF GLUCARATE TO 5-KETO-4-
DEOXY-D-GLUCARATE (5-KDGLUC) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: D-GLUCARATE = 5-DEHYDRO-4-DEOXY-D-GLUCARATE
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-1- SIMILARITY: BELONGS TO THE MANDELATE RACEMASE / MUCONATE
LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2000 (Rel. 40, Last annoctation update)
PROBABLE GLUCARATE DEHYDRATASE (EC 4.2.1.40) (GDH) (GLUCD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.7%; Score 37; DB 1; Length 376; 70.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                      SGD; SNOBLIG; ARGZ.
InterPro; IPR000453; --
InterPro; IPR000453; --
InterPro; IPR000453; --
InterPro; IPR000453; --
InterPro; IPR000787; --
INTER, PS00788; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.
INTERPRO; CHORISMATE_SYNTHASE_2; 1.
INTERPRO; ARGAIC AND A CHORISMATE_SYNTHASE_3; 1.
SEQUENCE 376 AA; 40838 MW; AF3AF65605B91E8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168;
MEDLINE=95219079; PubMed=7704254;
                                                                                                                                                                                                                          EMBL; X60190; CAA42745.1; -. EMBL; X998G0; CAA68214.1; -. EMBL; Z72670; CAA968G0.1; -. PIR; S17246; S17246. SGD; S0003116; ARO2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D30808; BAA06470.1; -. EMBL; Z99105; CAB12043.1; -. SubtiList; BG11161; gudD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ||||:| |
264 VSVPGSKHND 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VEVPGSQHID 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUDH_BACSU
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GUDH_BACSU
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALKTING ACTIVITY: HYDROLYSTS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDEDS IN BETA-D-GALACTOSIDES.
--- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
SUPRESSOR OF TUMORIGENICITY 14 (EC 3.4.21.-) (MATRIPTASE) (MEMBRANE-TYPE SRINE PROFESE 1) (MT-SP1).
ST14 OR PRES14 OR SNC19.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum). Bacteria; Firmicutes; Bacillus/Clostridium group; Thermoanaerobacter group; Thermoanaerobacter.
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153 NUCLEOPHILE (BY SIMILARITY).
85796 MW; FE011FF517E51DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 743;
Pred. No. 45;
2; Mismatches 3; Indels
                        Length 455
                                                                      1; Indels
                        ij
                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
                     Score 36; DB 1
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                    743 AA.
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PROSTER, PS00703; GLYCo_hydro_2; 1.
PROSTER, PS00719; GLYCOSYL_HYDROL_F2_1; 1.
Hydrolase; Glycosidase.
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54.5%;
                        58.1%;
75.0%;
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Best Local Similarity 54.5
Query Match
Best Local Similarity 75.0
Local 6; Conservative
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 33223 / 39E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                               |||| :||
64 EVPGGEHI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388
453
                                                                                                               2 EVPGSQHI 9
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Q9Y5Y6;
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P77989;
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CARBOHYD
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TRANSMEM
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GLS3_YEAST
   FITTE
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                                                                                                                                                                                                                                               Lin C.Y., Anders J., Johnson M., Dickson R.B.;
"Purification and characterization of a complex containing matriptase and a Kunitz-type serine protease inhibitor from human milk.";
J. Biol. Chem. 274:18237-18342(1999).
-1- FUNCTION: DEGRADES EXTRACELLULAR MATRIX. PROPOSED TO PLAY A ROLE IN BREAST CANCER INVASION AND METASTASIS. EXHIBITS TRYPSIN-LIKE ACTIVITY AS DEFINED BY CLEAVAGE OF SYNTHETIC SUBSTRATES WITH ARG OR LYS AS THE PI SITE.
                                                                     Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
"Molecular cloning of cDNA for matriptase, a matrix-degrading serine
protease with trypsin-like activity";
J. Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                          Takeuchi T., Shuman M.A., Craik C.S.;
"Reverse blochemistry: Use of macromolecular protease inhibitors to dissect complex blological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";
Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS50068; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 4.
Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUB 1.

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                           MEDLINE-99303581; PubMed-10373424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002172; -. Pfam; PF00057; Idl_recept_a; 4. Pfam; PF00089; trypsin; 1. Pfam; PF00431; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF118224; AAD42765.2; -. EMBL; AF133086; AAF00109.1; -. HSSP; P00763; 1DPO.
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000859; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            855
334
447
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524
560
603
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                                                                                                                                                                                                                                                                                                                                                                                                TRYPSIN FAMILY.
                                               SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                CHARACTERIZATION.
                                                                                                                                                                                                                                       PubMed=10373425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.302;
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214
340
452
487
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566
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UDP-GLUCOSE + (1,3-BETA-D-GLUCOSYL)(N) = UDP + (1,3-BETA-D-GLUCOSYL)(N+1).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: STRONG, TO GLSI AND GLS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE 1,3-BETA-GLUCAN SYNTHASE COMPONENT (EC 2.4.1.34) (1,3-BETA-D-
GLUCAN-UDP GLUCOSYLTRANSFERASE)
YMR306W OR YM9952.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Transferase; Glycosyltransferase.
                                                                                                                                                                                                                                                                        Gaps
                 CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTEWTIAL).
                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                             DB 1; Length 855;
52;
                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                26143132C01F99C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1785 AA
                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                               Score 36;
Pred. No. 5
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                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z49212; CAA89139.1; -. SGD; S0004923; YMR306W.
                                                                                                                                                                                                                                 55.68;
                                                                                                                                                                     94769
                                                                                                                                                                                                                               Query Match 58.1
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
851
656
711
711
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11323
11390
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                                                                                                                                                                  855 AA;
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370 IEVPNNQHV 378
                                                                                                                                                                                                                                                                                                                  . 1 VEVPGSQHI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLS3_YEAST
Q04952;
                   ACT_SITE
ACT_SITE
ACT_SITE
CARBOHYD
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RESULT 10 PHEB_PSESP

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PHEB.

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                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN-ATCC 15692 / PAO1 / H103;
MEDLINE-93051258; PubMed-1427017;
MHUANG H., Siehnel R.J., Bellido F., Rawling E., Hancock R.E.W.;
"Analysis of two gene regions involved in the expression of the imipenem-specific, outer membrane porin protein OprD of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                      Kirsten J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO YEAST YDL087C AND S.POMBE SPCC16A11.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last sentotation update)
HYPOTHETICAL 37.0 KDA PROTEIN B0495.8 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36977 MW; 000D2327621BFED0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 1;
Pred. No. 27;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q01609; Q911P9;
01-FEB-1995 (Rel. 31, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
HYPOTHETICAL PROTEIN PA2218.
      313 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEMS Microbiol. Lett. 76:267-274(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.5%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U21317; AAA62527.1; -. WormPep; B0495.8; CE01766. Hypothetical protein. SEQUENCE 313 AA; 36977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVPGSQHIDSQ 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
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                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kivisaar M., Kasak L., Nurk A.; "Sequence of the plasmid-encoded catechol 1,2-dioxygenase-expressing gene, pheB, of phenol-degrading Pseudomonas sp. strain EST1001."; Gene 98:15-20(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00775; Dioxygenase; 1.
PROSITE; PS00083; INTRADIOL_DIOXYGENAS; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Dioxygenase; Iron; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1-CATALYTIC ACTIVITY: CATECHOL + O(2) = CIS,CIS-MUCONATE.
-1-COFACTOR: FERRIC ION.
-1- PATHWAY: PHENOL DEGRADATION.
-1- SIMILARITY: BELONGS TO THE INTRADIOL RING-CLEAVAGE DIOXYGENASE
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                                                                                                                    Score 36; DB 1; Length 1785;
Pred. No. 1.2e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 56.5%; Score 35; DB 1; Length 302; Best Local Similarity 41.7%; Pred. No. 26; Matches 5; Conservative 3; Mismatches 4; Indels
1713 1733 POTENTIAL.
1785 AA; 207482 MW; 3475446DA46C6120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33362 MW; A86F17E68D1EAC3A CRC64;
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IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
CATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91192610; Pubmed=2013408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas sp. (strain EST1001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M57500; AAC64900.1; -.
                                                                                                                    58.1%;
54.5%;
                                                                                                                    Query Match 58.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pEST1412.
Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : || ||::|
227 ISAPGHQHLTTQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JN0143; JN0143.
HSSP; P00437; 3PCN.
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198
222
222
224
302 AA;
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                                                                                                                                                                                                                                                                                                  403 EWPGAQHLSSR 413
                                                                                                                                                                                                                                            2 EVPGSQHIDSQ 12
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P31019;
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SEQUENCE
TRANSMEM
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RESULT 11 YP68_CAEEL

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EMBL; D37929; BAA07149.1; -.
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      THIOETH
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   DR NO 
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Biochim. Biophys. Acta 1261:151-154(1995).
-!- FUNCTION: THIS IS A COPRER-CONTAINING OXIDASE THAT FUNCTIONS IN
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 22788 / RIB 128;
MEDLINE-95200965; PubMed-73753;
REDILINE-95200965; PubMed-73753;
MOLECULAR CLORING and nucleotide sequence of the protyrosinase gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOPAQUINONE + H(2)0.
COFACTOR: BINDS TWO COPPER IONS.
ENZYME REGULATION: ACTIVATED BY ACIDIFYING TREATMENT AT PH 3.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melO, from Aspergillus oryzae and expression of the gene in yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.5%; Score 35; DB 1; Length 371; 62.5%; Pred. No. 32; ive 2; Mismatches 1; Indels
"Complete genome sequence of Pseudomonas aeruginosa PAO1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R -> P (IN REF. 1).
R -> P (IN REF. 1).
A -> G (IN REF. 1).
D7EBOCCAC95A7CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYRO_ASPOR STANDARD; PRT; 539 AA.
000234;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1900 (Rel. 39, Last annotation update)
TYROSINASE (EC 1.14.18.1) (MONOPHENOL MONOOXYGENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMOTETRAMER.
PTM: THE N-TERMINAL IS BLOCKED.
SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 214064; CAA78447.1; -.
EMBL, AE00468; AAGG5606.1; ALT_INIT.
PTR; S23861; S23861.
                               opportunistic pathogen.";
Nature 406:959-964(2000).
-1- SIMILARITY: TO E.COLI YCJY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 VPGASHVD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VPGSQHID 10
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. B73;

MEDLINE-95357417; Pubmed=7630946;

Xu J., Pemberton G.H., Almira E.C., McCarty D.R., Koch K.E.;

Xu J., Pemberton G.H., Almira E.C., McCarty D.R., Koch K.E.;

"The Ivr 1 gene for invertase in maize.";

Plant Physiol. 108:1293-1294(1995).

-!- CATALTY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.

-!- SUBCELLULAR LOCATION: VACUOLAR.

-!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA-FRUCTOFURANOSIDASE 1.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                               Monooxygenase; Copper.
                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; Length 539;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                          Melain biosynthesis; Oxidoreductase; Monooxygenase; Cc
METAL 63 63 COPPER A (BY SIMILARITY).
METAL 84 COPPER A (BY SIMILARITY).
METAL 290 COPPER A (BY SIMILARITY).
METAL 290 COPPER B (BY SIMILARITY).
METAL 294 294 COPPER B (BY SIMILARITY).
METAL 333 333 COPPER B (BY SIMILARITY).
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                                                                                                                                                                                                                                                                    BY SIMILARITY
MM;
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                                                                                                                                 63
984
2990
2990
333
84
60604 h
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Best Local Similarity 54...
6; Conservative
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139
165
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294
333
333
82
539 AA;
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Multigene family.
SIGNAL
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165
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P49175;
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STANDARD;
                                                                                                                                                                                                                                           Mus musculus (Mouse).
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589
733
820
960 AA;
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Matches 6; Conserv
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PGDQHDDAQ 32
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                     FGD1_MOUSE
P52734;
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DOMAIN
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DOMAIN
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                                                                   RESULT 16
FGD1_MOUSE
                   24
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-1- SUBCELLULAR LOCATION: THE CHITIN SYNTHASE FAMILY. SUBFAMILY CLASS
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92090722; PubMed-1836444;
Yarden O., Yanofsky C.;
"Chitin synthase I plays a major role in cell wall biogenesis in Neurospora crassa.";
Genes Dev. 5:2420-2430(1991).
-!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
-!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
-!- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + [1,4-(N-ACETYL-BETA-D-BETA-D-BETA-D-GLUCOSAMINYL)](N) = UDP + [1,4-(N-ACETYL-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BE
                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CHITIN SYMMHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3) (CLASS-III CHITIN SYNTHASE 3).
   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002923; -.
Pfam; PF01644; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                     DB 1; Length 670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 960; 92;
                                                                                                                                                       Indels
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; 633A2107319BF447 CRC64;
                                                                   DEDE0989C7E6AEB0 CRC64;
   (GLCNAC. . .) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
960 AA
                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                    Score 35;
Pred. No. 6
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.5%; Score 35;
66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                            PRT;
                                                                     Œ.
                                                                                                                    56.5%;
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                                                                   71932
                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          591
650
685
737
765
867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUCOSAMINYL)](N+1)
                                                                                                                                                                                                                  61 VTVLASQHVDGQ 72
                                                                                                                                                                                      1 VEVPGSQHIDSQ 12
275
518
595
639
670 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A41638; A41638
                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                            CHS3_NEUCR
P29070;
                                CARBOHYD
CARBOHYD
CARBOHYD
                   CARBOHYD
                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                          RESULT 15
CHS3_NEUCR
                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 dysplasia (Fgd1) gene.";
mamm. Genome 6:658-651(1995).
-!- FUNCTION: ACTIVATES THE RAS-LIKE FAMILY OF RHO- AND RAC PROTEINS
BY EXCHANGING BOUND GDP FOR FREE GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE-96081343; PubMed-8535076;
Pasteris N.G., de Gouyon B., Cadle A.B., Campbell K., Herman G.E.,
                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                   01-OCT-1996 (Rel. 34, Last sequence update)
Last annotation update)
PUTATIVE RHO/RAC GUAININE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF)
(FACIOGENITAL DYSPLASTA PROTEIN HOMOLOG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 960;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: CYTOPLASNIC (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
-!- SIMILARITY: CONTAINS 2 PH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO-RICH.
SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guanine-nucleotide releasing factor; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00621; RhoGEF; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50003; PH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2H2-TYPE.
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01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U22325; AAA96001.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.5%;
75.0%;
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InterPro; IPR000219; -
InterPro; IPR000826; -
InterPro; IPR001849; -
InterPro; IPR01849; -
Pfam; PF01163; FYVE; 1.
Pfam; PF00169; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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FGD1_HUMAN
ID FGD1_HUMAN
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                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
MEDLINE-98232498; PubMed-9564035;
Inohara N., Koseki T., Chen S., Wu X., Nunez G.;
"CIDE, a novel family of cell death activators with homology to the 45 kDa subunit of the DNA fragmentation factor.";
EMBO J. 17:2526-253311998).
                                                         01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
CELL DEATH ACTIVATOR CIDE-A (CELL DEATH-INDUCING DFFA-LIKE EFFECTOR
                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.8%; Score 34; DB 1; Length 219; 71.4%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 CIDE-N.
24686 MW; 05F704823CE71C0E CRC64;
  Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  -i - FUNCTION: ACTIVATES APOPTOSIS.
-i - SUBUNIT: INHIBITED BY DFFB.
-i - SIMILARITY: CONTAINS 1 CIDE N DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                    01-OCT-2000 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF041378; AAC34987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02017; CIDE-N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 1.6.99.3).
AT4G02580 OR T10P11.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 1
219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||||:
109 MPGSQHV 115
                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VPGSQHI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 604440;
CIDA_HUMAN
O60543;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                            CIDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUHM ARATH
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    ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: FACIOGENITAL DYSPLASIA (AARSKOG-SCOTT SYNDROME) IS A RARE MULTISYSTEMIC DISORDER CHARACTERIZED BY DISPROPORTIONATELY SHORT STATURE, AND BY FACIAL, SKELETAL, AND URGENITAL ANOMALIES.
SIMILARITY: CONTAINS 1 DEL-HOMOLOGY DOMAIN (DH).
SIMILARITY: CONTAINS 2 PH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CYPOPLASMIC (BY SIMILARITY).

TISSUE SPECIFICITY: FETAL HEART, BRAIN, LUNG, KIDNEY, PLACENTA,
AND LESS IN LIVER; ADULT HEART, BRAIN, LUNG, SKELETAL MUSCLE, AND
LESS IN PANCREAS AND LIVER.
                                                                                                                                                                                                                                                             TISSUE-Craniofacial;
MEDLINE-95042764; PubMed-7954831;
Pasteris N.C., Cadle A., Logie L.J., Porteous M.E.M., Schwartz C.E.,
Stevenson R.E., Glover T.W., Wilroy R.S., Gorski J.L.;
"Isolation and characterization of the faciogenital dysplasia
(Aarskog-Scott syndrome) gene: a putative Rho/Rac guanine nucleotide
exchange factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Cell 79:669-678 1994).
-1- FUNCTION: ACTIVATES THE RAS-LIKE FAMILY OF RHO- AND RAC PROTEINS BY EXCHANGING BOUND GDP FOR FREE GTP.
                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence.update)
01-0CT-2000 (Rel. 40, Last annotation update)
PUTATIVE RHO/RAC GUANINE NUCLECTIDE EXCHANGE FACTOR (RHO/RAC GEF)
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF722598853A685A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO-RICH.
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50003; PH_DOMAIN; 2.
Guanine-nucleotide releasing factor; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1;
Pred. No. 92;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
                                                                                                   (FACIOGENITAL DYSPLASIA PROTEIN)
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75.0%;
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InterPro; IPR000306; ...
InterPro; IPR00082; ...
InterPro; IPR001849; ...
Pfam; PF01163; FYVE; I...
Pfam; PF00169; PH; 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00621; RhoGEF; 1
                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
179
590
734
821
961 AA;
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Best Local Similarity
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE
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Gaps

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STRAIN-CV. COLUMBIA;
MEDLINE-20083488; Pubmed=10617198;
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stickema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
Weichselgartner M., de Simone V., Obernaier B., Mache R., Mueller M.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schnidtheini T.,
Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT PRECURSOR (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Magnoliophyta; Eussicaceae; Arabidopsis.
NCBL_TaxID=3702;
244 AA
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DOMAIN DOMAIN

Pfam;

DOMAIN

Matches

à g CIDA_HUMAN

RESULT

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RA VOS P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
Ra Jangham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
Ra Braeken M., Weltjens I., Voet M., Bastlaans II., Aert R., Defoor E.,
Ra Weitzenegger T., Edrhe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkee W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Limberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Bertett A., Rajandream M.-A., Lyne M., Benez V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T. -H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T. -H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T. -H.,
RA Borkova D., Bloecker H., Schaffer M., Rechmann S.,
Ra Borkova D., Bloecker M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fruchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Felber R.,
Rackonabl S., Hiller R., Schmidt W., Lecharny A., Robor S.,
Ra Berez-Perez A., Purnelle B., Bent E., Johnson S., Taccon D., Josse T.,
Ratishman D., Haase D., Lemcke K., Mewes H. W., Stocker S.,
Ratishman D., Haase D., Lemcke K., Mewes H. W., Stocker S.,
Rackorlin P., Bevran M., Wilson R.K., Mewel B., Stocker S.,
Rateralle D., Dedhia W., Marison R.K., Mewel S., Grock M., Habermann K.,
Ramcell L., Schwarz S., Scholler P., Haber S., Schot M., Abbert A., Johnson D.,
Ramching T., Kalicki J., Graves T., Harmon G., Edwards J.,
Rateralle P., Dedhia W., Milson R.K., Hone S., Gotte R., Johnson D.,
Ramch J., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Ramer J., Bentley D., Pulton B., Miller N., Greco T., Layman D.,
Ramer J., Spleth J., Ryan E., Poord S., Sott R., Anderson J., Spleth J., Ryan E., Johnson D.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRION (POTENTIAL).
NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan, PF01257; complex1_24kD; 1.
PROSITE; PS01099; COMPLEX1_24k; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON-SULFUR (2FE-2S) (POTENTIAL).
IRON-SULFUR (2FE-2S) (POTENTIAL).
IRON-SULFUR (2FE-2S) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC002330; AAC78260.1; -. EMBL; AL161494; CAB80751.1; -.
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124
160
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124
160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea, Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
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 IRON-SULFUR (2FE-2S) (POTENTIAL).
27C95BF5884B12AC CRC64;
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Pred. No. 49;
4; Mismatches 2; Indels
                                                            Length 244;
                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00423; CELLDVISFTSZ.
PRINTS; PR01161; TUBULIN:
PROSITE; PR00227; TUBULIN: 1.
Cell division; Septation; GTP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND 99 107 GTP (POTENTIAL)
SEQUENCE 365 AA, 39957 MW; ACC31761552F0CC5 CRC64;
                                                         Score 34; DB 1;
Pred. No. 31;
                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                 365 AA.
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                                                                                         1; Mismatches
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 164 II
27182 MW;
                                                                                                                                                                                                                                                            01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last seq
01-OCT-2000 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last seqq)
01-0CT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%;
45.5%;
                                                           54.8%;
                                                           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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195 IDVPGEQTLDA 205
164 1/
244 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-29292;
                                                                                                                       4 PGSQHIDS 11
                                                                                                                                         1 | | | | : | |
20 PTSQHLDS 27
                                                                                                                                                                                                                                                                                                                          FTSZ3 OR PAB1820
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ORSAY;
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O59060;
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 METAL
SEQUENCE
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                                                                                                                                                                                                                                                 Q9V0H5;
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FTZ3_PYRHO
AC 059060.
DT 01-0CT
DT 01-0CT
DT 01-0CT
DE CELL DC
GN FTSZ3.
OS PYROCO
OC AFCEN
OX NCBL_AC
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FTZ3_PYRAB
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SUBCELLULAR LOCATION: NUCLEAR.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                  Pfam; PF00046;
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                                                                                                                                                                                                                                                                                                                                                                                        DNA_BIND
SEQUENCE
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AROC_NEUCR
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                                             Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

BEDILINE-96272167, Pubmed-8670808;

Hahn M., Jackle H.;

"Drosophila goosecoid participates in neural development but not in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     body axis formation.";
EMBO J. 15:3077-3084(1996).
-!- FUNCTION: APPEARS TO REGULATE REGIONAL DEVELOPMENT OF SPECIFIC
TISSUES. CAN RESCUE AXIS POLARITY IN UV-RADIATED XENOPUS
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                  54.8%; Score 34; DB 1; Length 365; 45.5%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goriely A., Stella M., Coffinier C., Kessler D., Mailhos
Dessain S., Desplan C.;
                                                                                                                                                                                                                                                                                                                                     Septation; GTP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                 GTP (POTENTIAL).
DC987E91C761F5B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A functional homologue of goosecoid in Drosophila."; Development 122:1641-1650(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HOMEOBOX PROTEIN GOOSECOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 49;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                               MEDLINE=98344137; Pubmed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96202483; PubMed-8625850;
                                                                                                                                                                                                                                                                        EMBL; AP000006; BAA30441.1; -.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 365 AA; 40118 MW;
                                                                                                                                                                                                                                                                                                                        PROSITE; PS00227; TUBULIN; 1.
                                                                                                                                                                                                                                                                                                             Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 54.8
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                    InterPro; IPR000217; -. InterPro; IPR003008; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 IDVPGEQTLDA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VEVPGSQHIDS 11
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 66
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                                                                                                                                                                                                                                                                                                                                     Cell division;
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P54366;
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TISSUE SPECIFICITY: IN EARLY EMBRYO DEVELOPMENT, EXPRESSION CONFIRMED TO TWO REGIONS; A HORSESHOR-LIKE PATTERN ACROSS THE DORSAL SIDE WHICH IS DESTINED TO FORM THE BRAIN HEALSPHERES AND A SECOND DOMAIN WHICH INVAGINATES INSIDE THE STOWODEUM AND WHICH, IS
                                                                                                                                                                                                                                        -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: 5-0-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE -
CHORISMATE + ORTHOPHOSPHATE.
COFACTOR: REDUCED FLAVIN.
PATHMAX: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                          FATED TO FORM THE FOREGUT, RING GLAND AND STOMATOGASTRIC NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crassa.";
J. Biol. Chem. 270:20447-20452(1995).
J. Biol. Chem. 270:20447-20452(1995).
-!- FUNCTION: BIFUNCTIONAL ENZYME THAT POSSESSES CHORISMATE SYNTHASE
                                                                                                                                                              SYSTEM (SNS).
SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
"BICOID" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bifunctional chorismate synthase/flavin reductase from Neurospora
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Nuclear protein; DNA-binding; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE-95386486; PubMed-7657620;
Henstrand J.M., Amrhein N., Schmid J.;
"Cloning and characterization of a heterologously expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 419;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-SER.
POLY-ALA.
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0010323; Gsc.
InterPro; IPR001356; -.
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199
345
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286
3
419 AA;
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PS00300;
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P16872;
                                                                                                                                                                                                           NP_BIND
SEQUENCE
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CARBOHYD
      PROSITE;
                                                                                                                                      NP_BIND
NP_BIND
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                                                                            DOMAIN
                                                                                                       DOMAIN
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ID A MOUSE

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      KW KW KW FT FT FT FT SO
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1 FUNCTION: BINDS TO THE SIGNAL SEQUENCE OF PRESECRETORY PROTEIN WHEN THEY EMERGE FROM THE RIBOSOMES (BY SIMILARITY).

-1 SUBBUNIT: ARCHAREAL SIGNAL RECCGNITION PARTICLE CONSISTS OF A 7S RNA MOLECULE OF 300 NUCLEOTIDES AND TWO PROTEIN SUBUNITS: SRP54 AND SRP19 (BY SIMILARITY).

-1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-1 DOMAIN: HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE 7S RNA IN PRESENCE OF SRP19 AND ALSO BINDS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL SEQUENCE (BY SIMILARITY). SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
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InterPro; IPR000453; -.
Pfam; PF01264; Chorismate_synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.
Lyase; Aromatic amino acid biosynthesis; Oxidoreductase; NADP; Multifunctional enzyme.
NP_BIND 260 291. NADPH (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.8%; Score 34; DB 1; Length 432; 77.8%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
-!- SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 291 NADPH (POTENTIAL).
432 AA; 45967 MW; 201A0B525C406F0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
SIGNAL RECOGNITION 54 KDA PROTEIN (SRP54).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20479972; PubMed-11029001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.0.
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 EVPGSIHND 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EVPGSQHID 10
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ID SR54_THEAC
AC Q9HKT0;
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                                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE-90199875; Pubmed-2317865;
GOODWIN R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A.,
Gimpel S., Cosman D., Dower S.K., March C.J., Namen A.E., Park L.S.;
"Cloning of the human and murine interleukin-7 receptors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i - FUNCTION: RECEPTOR FOR INTERLEUKIN-7.
-i - SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
-i - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i - TISSUE SPECIFICITY: SPLEEN; THYMUS; AND FETAL LIVER.
-i - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i - SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPROUZ-2,
InterPro; IPRO0177; -.
InterPro; IPRO02465; -.
Pfam; PF00041; fn3; --
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SER/THR-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERLEUKIN-7 RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     demonstration of a soluble form and homology to a new receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last anotation update)
INTERLEUXIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA).
                                                                                                                                                                                                                                                            Length 456;
                                                                                                                                                                                                                                                                                                              1; Indels
                DESTRICT: GTP-binding; RNA-binding.
289 G-DOMAIN (BY SIMILARITY).
456 M-DOMAIN (BY SIMILARITY).
111 GTP (BY SIMILARITY).
188 GTP (BY SIMILARITY).
245 GTP (BY SIMILARITY).
545 GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                         Score 34; DB 1;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 AA.
                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                         54.8%; 75.0%;
SRP54; 1.
                                                                                                                                                                                                                                                         Query Match 54.8
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
239
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189
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                        Signal recognition
                                                                                                                                                                              456 AA;
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353 IPGSOKID 360
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104
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128
184
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 115 115 N-LINKED (GLCNAC. ..) (POTENTIAL).
177 N-LINKED (GLCNAC. ..) (POTENTIAL).
282 282 PHOSPHORYLATION (BY PKC) (POTENTIAL).
459 AA; 51704 MW; CC06ASCE95543849 CRC64;
                                                                                                             Query Match 54.8%; Score 34; DB 1; Length 459; Best Local Similarity 66.7%; Pred. No. 63; Matches 6; Conservative 2; Mismatches 1; Indels
CARBOHYD
CARBOHYD
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Search completed: July 16, 2001, 16:44:03 Job time: 462 sec

1 VEVPGSQHI 9. :|| ||||: 46 LEVDGSQHL 54

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Oge226 helicoverpa

Og9226 helicoverpa

Og9429 hepatitis b

Ogyu09 hepatitis b

Ogduh1 hepatitis b

Ogdun1 hepatitis b

Ogdun1 hepatitis b

Ogmn7 hepatitis b

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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE=95303036; PubMed=7783690;
Nakashima K., Eguchi Y., Nakasone N.;
"Characterization of an enterotoxin produced by Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiol. Immunol. 39:87-94(1995).
HSSP: P01556; 1XTC.
InterPro; IPR001835; -.
Pfam: PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          057193,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA TOXIN B PROTEIN (CTB) PRECURSOR (CTB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA-LIKE ENPEROTOXIN B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                              09E226
09S079
09S079
09S079
09DUH5
09DUH1
091529
09DUH1
091520
097704
099V9U6
095V9U6
095V9U6
095V9U6
095V9U6
095V9U6
004636
Q9HB36
Q9XD79
Q9V7M7
Q9U0W5
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O42099
O01797
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Best Local Similarity 100.
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12
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SEQUENCE.
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AC 05
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Q5635 vibrio chol
Q9r015 vibrio chol
Q9r015 vibrio chol
Q9r025 streptomyce
Q3135 bacillus ce
Q9nqq6 homo sapien
Q9r128 streptomyce
Q9mal6 arabidopsis
Q9qQ4 homo sapien
Q9rv17 deinococcus
Q9rv17 deinococcus
Q9yv17 deinococcus
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014347 schizosacch
080418 nicotiana t
099987 homo sapien
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022511 vitis vinif
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                 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Q9RP15
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sp_unclassified:*
sp_vertebrate:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_phage:*
sp_plant:*
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Maximum DB seq length: 2000000000
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Drosophia melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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STRAIN-Y. CHE BY SP.
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STRAIN-Y. CHE BY SP.
AShburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Celniker S., Rubin G.M.;
An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea."; Misalamurhag Hoiji 35:205-210(1999).
EMBL; ARI75703; AAD51360.1; -. HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 62; DB 2; Length 124; Best Local Similarity 100.0%; Pred. No. 0.00037; Matches 12; Conservative 0; Mismatches 0; Indels
                                                            Length 124;
                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001835; -.
Pfam; PF01376; EnterPotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRINTS; PR0772; ENTEROTOXINB.
SEQUENCE 124 AA; 13905 WW; 23BF83FFF793E5B9 CRC64;
13871 MW; 3F87B2F297953179 CRC64;
                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA ENTEROTOXIN B-SUBUNII.
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
                                                      Query Match
100.0%; Score 62; DB 2; Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 12; Conservative 0; Mismatches 0;
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                                                                                               SEQUENCE FROM N.A.
STRAIN=CLASSICAL STRAIN 569B;
MEDLINE=9135224; Pubmed=1883840;
Dams E., De Wolf M., Dierick W.;
Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical strain 569B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparison of cholera toxin genes (ctxAB) of non-Ol vibrio cholerae strains 854 (Ol39-bengal) and S7 (O37) from two outbreaks."; Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases. HSSP; PO1556; 2CHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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Yamamoto K., Do V.G., Xu M., Iida T., Miwatani T., Albert M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 62; DB 2; Length 124; Best Local Similarity 100.0%; Pred. No. 0.00037; Matches 12; Conservative 0; Mismatches 0; Indels
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X58785; CAA41591.1; -.
EMBL; U25679; AAC34728.1; -.
EMBL; A00931; CAA00098.1; -.
HSSP; P01556; ZCHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA TOXIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA.
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Shi C., Cao C., Zhang J., Ma Q.;
Chin. Biochem. J. 9:395-399(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR01835; -.
Ffam: PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
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Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
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STRAIN=CLASSICAL BIOTYPE 569B;
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Vibrio cholerae.
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REPRESENT REPRES

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Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for integrated Molecular analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN*ATCC 10987;
Kolsto A.B., Okstad O.A., Lindback T., Hegna I., Lagreid A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 62.9%; Score 39; DB 4; Length 192; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rishovd A.L.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y11217; CAA72103.1; -.
InterPro; IRR000212; -.
Pfam; PF00580; UVrD-helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Pluvinet R., Sumoy L.; Pluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL389957; CAB97531.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 AA; 21609 MW; 04A7AE8CB344F213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 AA; 29212 MW; 24392E11338D99EA CRC64;
                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
ATP-DEPENDENT NUCLEASE SUBUNIT A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
LLPL, LCAT-LIKE LYSOPHOSPHOLIPASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 2;
Pred. No. 11;
2; Mismatches
                                                                                                                                                      254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 AA
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.5%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 64.5
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: |||||| |
35 IDEPGSQHIRKQ 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
      204 VEVPGTDHTD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                           Bacillus cereus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
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SEQUENCE
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09NPQ6;
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                                                                                            RESULT
031335
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                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Colliker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

Colniker S.E., Galbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

Buttenhoff C., Champe M., Chavez C., Chew M., Cicsiolka L., Doyle C.M.,

Ratfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

Lewis S., Li P., Lomottan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

Sethi H., Snir E., Syirskas R.R., Wan K.H., Weinburg T., Zhang R.,

Li Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AE001408; AAF44847.1; --

Riybase; FSH010028907; BG:DS01514.3.

W Hypothetical protein.
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL031184; CAA20190.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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0
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Pred. No. 4.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy L., Harris D.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002502; -.
Pfam; PF01510; Amidase_2; 1.
Hypothetical protein.
SEQUENCE 242 AA; 26018 MW; 6DD10FF18A2EC544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TTEMBLEE]. 08, Last sequence update) 01-MAY-2000 (TTEMBLEE]. 13, Last annotation update) HYPOTHETICAL 26.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.48;
Genetics 153:179-219(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VEVPGSQHIDS 11
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Chol E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ACO10793; AAF68106.1; -. ERGURE 260 AA; 29128 MW; B149F22073AA0B92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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  \mathrm{I.'}^{\circ}; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Ecker J.R.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31016 MW; ACCC5E1680D7A720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TIEMBLIEL. 13, Last sequence update) 01-MAR-2001 (TIEMBLIEL. 16, Last annotation update) HYPOTHETICAL 31.0 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 10;
Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.9%; Score 39; DB 66.7%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09RvJ7 PRELIMINARY; PRT; 09RvJ7; 01-MAY-2000 (TEMBLEEL: 13, Created) 01-MAY-2000 (TEMBLEEL: 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.9%;
50.0%;
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InterPro; IPR003386; -.
Pfam; PF02450; LACT; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.9
Best Local Similarity 50.0
Matches 6; Conservative
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272 AA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VEVPGSQHIDSQ 12
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                           SEQUENCE FROM N.A.
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246 ELPGSEHIE 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q9UG04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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Kinashi H., Hopwood D.A.;
Radenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coclicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; ALJ33210; CAB61584.1;
InterPro; IPR002502;
Pfam; PF01510; Amidase_2; 1.
SEQUENCE 201 AA; 22749 MW; BBEF477E06A20468 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Bragnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Len C., Liu A., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 2; Length 201;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
Oliver K., Harris D.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
F20B17.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AA.
                                                                                                   201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                           Created)
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
MEDLINE=97000351; Pubmed=8843436;
                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14, PUTATIVE AMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                            Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
166 ELPGSEHIE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||| | | |
|176 EVPGSDHTD 184
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EVPGSQHID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker J.R.;
                                                                                                09RJZ8
                                                                                                                        09RJZ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09MA16
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                                                        RESULT
Q9RJZ8
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Oryza sativa (Rice).
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.
NCBI_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A); TISSUE-FRUIT;
Cassol T., Adams D.O.;
Submitted AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
SASANI T., MAISUNGOO I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 10; Length 428; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTATHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT)
                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00390; 1ALG.
Mendel; 26381; Vitvi;1190;26381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      022511;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000103; -.
InterPro; IPR001100; -.
InterPro; IPR001327; -.
Pfam; PF00070; pyr_redox; 1.
                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASS-I.
EMBL; AF019907; AAB70837.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.6
Matches 7; Conservative
                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitis vinifera (Grape).
                                                                                                                                         ESTS AU056822(S20908).
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187 KVPGGWHIDGQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                        clone: P0041E11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                     Q9LGM2;
Q9LGM2;
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022511
                    14
                    RESULT
                                        O9LGM2
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                                                                                                                                                    MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBL_TaxID=1299;
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MEDLINE=99194552; PubMed=10092508;
Taniyama Y., Shibata S., Kita S., Horikoshi K., Shirafuji H.,
Sumino Y., Fujino M.;
"Cloning and expression of a novel lysophospholipase which
structurally resembles lecithin cholesterol acyltransferase.";
EMBL, AB017494; BAA76877.1; -
InterPro; IPR003366; -
Pfam; PF02450; LACT; 1.
                                                                                                                                                                                                                                                                                                 "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.9%; Score 39; DB 2; Length 353; 75.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.9%; Score 39; DB 4; Length 412; 66.7%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                INTEFFIC, AFANOSCOL,
PFOMIS PROIDING: FMN_AMPROXY_ACID_DH; 1.
PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
SROHFNICE 353 AA; 37877 MW; 14FB78FAEZE18C8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 AA; 46657 MW; 1FEA8A5783AF050A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
LCAT-LIKE PROTEIN (LLPL).
   Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 AA.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 28;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                             Science 286:1571-1577(1999).
EMBL: AE001954; AAF10604.1;
HSSP: P05414; 1GOX.
01-MAR-2001 (TrEMBLrel. 16, (S)-2-HYDROXY-ACID OXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.9
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000262; -. InterPro; IPR003009; -.
                                                     Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
-has 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|||:||:
386 ELPGSEHIE 394
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EVPGSQHID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 VPGSEHLD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VPGSQHID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                   radiodurans R1
                                                                                                                                                                                                                                                                                  Fraser C.M.;
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Q9Y2B3 RESULT 13

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RA Adman B.D. Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adman W.D. Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adman W.D. Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., I. P.W. Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-L., Blazej R.G., Cham D. X.,

RA Barli J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Baldwin D.,

RA Bartis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Dockon R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk

RA Dockon R., E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk

RA Dockon R., Cong F., Gorrell J.H., Gu Z., Gunn P., Harris R.C.,

RA Harris N.L., Harvey D., Helman T.J., Wein M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Helman T.J., Wein M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Mallshina N.V. Mobarry C., Morris J., Mornis J., Maltshina N.V. Mobarry C., Morris J., Puri V., Resee M.G.,

RA Reinert K., Remington K., Sunders R.D., Puri V., Resee M.G.,

RA Reinert K., Remington M., Sunders R.D., Puri V., Resee M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shilt T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan H.Y.E., Harris S.J., O'Kane C.J.; Identification and characterization of kraken, a gene encoding a putative hydrolytic enzyme in Drosophila melanogaster."; Gene 222:195-201(1998).
                                                                                                                                                                  ä
                                                                                                                                     DB 10; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE SERINE HYDROLASE (EC 3.1.-.-) (KRAKEN PROTEIN).
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDEDTASEI.
PRINTS; PR00469; PNDEDTASEII.
PROSTITE; PS00076; PYRIDINE_REDOX_1; 1.
FAD; Flavoprotein; Oxidoreductase; Redox-active center.
                                                                                        565 AA; 60695 MW; B26113AE09A121DE CRC64;
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                 331 AA
                                                                                                                                   62.1%; Score 38.5; 172.7%; Pred. No. 48;
                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99051329; PubMed-9831651;
                                                                                                                                   Query Match 62.1
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                             |:|||:| ||||
239 EIPGSEHAIDS 249
                                                                                                                                                                                            2 EVPGSQH-IDS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     KRAKEN OR CG3943.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea; Dro
                                                                         NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                    RESULT 16
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Woodage T., Worley K.C., The G., Zhao Q., Zhao Q., Zhao M., Zhou X., Zhu S., Zhao M., Zhou X., Zhu S., Zhu X., Smith H.O.,
R. Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
R. Zheng X.H., Wyers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
Science 28:2185-2195(2000)
L. FUNCTION: MAY HAVE A ROLE IN DETOXIFICATION AND DIGESTION DURING
EMBRYGGENESIS AND LARVAL DEVELOPMENT.
I. AT STAGE II, EXPRESSION IS CONCENTRATED IN THE END OF
EMBRYGGENESIS, EXPRESSION IS CONCENTRATED. PHARYNA,
POSTERIOR SPIRACLES AND ANTERIOR EDGE OF MIDGUT. AT THE END OF
EMBRYGGENESIS, EXPRESSION IS CONFIRED TO GASTRIC CAECAE, DURING
THIRD INSTAR LARVAE, EXPRESSED AT LOW LEVELS IN GASTRIC CAECAE,
MIDGUT AND HINDGUT AND HIGH LEVEL IN FAT BODY.
C. -- DEVELOPMENTAL STAGE: PROBABLY EXPRESSED BOTH MATERNALLY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H., Duesterhoeft A.; Submitted (JuL-1997) to the EMBL/GenBank/DDBJ databases.
--i- FUNCTION: Z-DNA BINDING PROTEIN. COULD BE INVOLVED IN CHROMOSOME ORGANIZATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2YGOTICALLY.
SIMILARITY: WERK, TO FAMILY OF ESTERASES THAT GROUPS TOGETHER PSEUDOMONA TROPINESTERASE, DMPD; TODE AND XYLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detoxification; Developmental protein; Digestion; Hydrolase; Serine esterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 BY SIMILARITY.
37093 MW; 1FE39BC42AED4E69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TIEMBLEEL. 06, Created)
01-JUN-1998 (TIEMBLEEL. 06, Last sequence update)
01-MAR-2001 (TIEMBLEEL. 16, Last annotation update)
PUTATIVE ZUOTIN-LIKE PROTEIN C30D10.01 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
EMBL; 297992; CAB10796.1; -.
HSSP; P25685; IHDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.7%; Score 37; DB Best Local Similarity 66.7%; Pred. No. 52; Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ000516; CAA04153.1; -.
EMBL; AE003588; AAF51445.1; -.
FlyBase; FB900020545; kraken.
InterPro; IPR000073; -.
InterPro; IPR000379; -.
InterPro; IPR000379; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001623; -. Pfam; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 VEVPGTHHL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VEVPGSQHI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-4896
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334 VHTPNSQKVDSQ 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           004636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   004636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
004636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HB36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanaka-Ueguchi M., Itoh H., Oyama N., Koshioka M., Matsuoka M.;
"Over-expression of a tobacco homeobox gene, NTH15, decreases the
expression of a gibberellin biosynthetic gene encoding GA 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
SMART; SM00271; DnaJ; 1.
Hypothetical protein; Chaperone; DNA-binding; Nuclear protein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 59.7%; Score 37; DB 10; Length 367; Best Local Similarity 87.5%; Pred. No. 58; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                            Score 37; DB 3; Length 354;
Pred. No. 56;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AB016084; BAA31690.1; -. Mendel; 31081; Nicta; 2972;31081.
                                                                                                   DNAJ-LIKE.
ALA/LYS-RICH.
; 6071B58A3B60F558 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00671; Fe_Asc_oxidored; 1.
SEQUENCE 367 AA; 42170 MW; 923BC90B3BBBAC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-1997 (TIEMBLrel. 03, Created)
01-JAN-1998 (TFEMBLrel. 05, Last sequence update)
01-WAR-2001 (TFEMBLrel. 16, Last annotation update)
VRK2, COMPLETE CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         367 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LIVER;
MEDLINE-98008921; PubMed=9344656;
Nezu J., Oku A., Jones M.H., Shimane M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                              40290 MW;
                                                                                                                                                                                                            59.7%;
                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002419; -.
                                                                                       1
81
                                                                                                                             267
                                                                                                   10
217
354 AA;
                                                                                                                                                                                                                                                                                                                  : | | :: |: | | 283 DVPSAEHVDS 292
                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                          2 EVPGSQHIDS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 EVPSSQHI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVPGSQHI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTC16 PROTEIN.
                                                                                                                           DOMAIN
SEQUENCE
                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            080418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        099987;
                                                                                                                                                                                                                                                                                                                                                                                                                                       080418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     099987
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080418
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1099987
AC 099987
DT 01-7AN DT 01-7A
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"Identification of two novel human putative serine/threonine kinases, VRK1 and VRK2, with structural similarity to vaccinia virus BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                    PROSITE; PSO0069; pKinase; 2.
PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
SMART; SM00108; PROFEIN_KINASE_ST; 1.
SMART; SM0020; S_TKC; 1.
ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 508 AA; 58126 MW; 157FBF6F48511AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 508
                                                                      Genomics 45:327-331(1997).
-1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL, AB000450; BAA19109.1; -.
HSSP: Q06486; 1CKI.
InterPro; IPR00719; -.
InterPro; IPR007290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Miller N., Beck C., Kramer J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (101-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF007270; AAB61058.1; -
Mendel; 17174; Arath;2663;17174.
InterPro; RR000679; -
Ffam; PF00320; GATA; 1.
PROSITE; PS50114; GATA, ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00401; ZnF_GATA; 1.
SEQUENCE 550 AA; 60856 MW; 488A05F20846091D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILARITY TO GATA-TYPE ZINC FINGERS.
A_IGO02P16.9.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 4;
Pred. No. 82;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB
Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HB36; PRELIMINARY; PRT; Q9HB36; 01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthand J.R., Yandell M.D., Zhang O., Chen L.X.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Baater E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Belshakov S.,
Borkova D., Botchan M.R., Bouck J., Exokatein P., Bolshakov S.,
Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chanfra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Belcher A., Deng Z., Mays A.D., Dev I., Dletz S.M.,
RA Goog F. Delcher A., Deng Z., Mays A.D., Dev I.D., Dletz S.M.,
RA Good R., Cong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser R.,
A Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibeywam C.,
Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Lasko P., Lel Y., Levitsky A.A., Li J., Ul Z., Liang Y., Lin X.,
Liu X., Matterla B., McIntosh T.C., McLender B., McPherson D.,
McIntan B.E., Rodirac C.D., Kraft C., Morris J., Woshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Replace D., Stafer E., Pollard J., Purl, Weissenbach J.,
Ra Spiere E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Sylskas R., Tector C., Turner R., Venter E., Wang A., K., Smith H.O.,
Raben D. R., Woodage T., Worley K.C., Wu D., Yang G., Zhao O., Zheng L.,
Rhillams S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao O., Zheng L.,
Rhenger D., Zhao W., Wooday T., Zhang G., Shao O., Zhao O., Z
                                                                                                                                                                                                                                 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UOW5 PRELIMINARY; PRT; 389 AA.
09UOWS;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
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94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36;
Pred. No.
                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAY-2000 (TrEMBLrel. 13, Last and
CG7750 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003807; AAF58021.1; -
FlyBase; FBgn0034107; CG7750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.1%;
54.5%;
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348 ELPGPQHKETO 358
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9U0W5
ID Q9
AC Q9
DT 01
         DDT TE THE TEACH TO THE TEACH THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=86383;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last aennotation update)
4-CARBOXYMUCONOLACTONE DECARBOXYLASE/3-OXOADIPATE ENOL-LACTONE
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Cao J., Fan W., Zheng S.;

Genomic analysis of a novel human serine protease SNC19.";

Submitted (JUW-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF283256; AAG13949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2; Length 373;
Pred. No. 92;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.
EMBL; AF109386; AAD40815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F6A7468C1B26B64F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 AA; 39583 MW; F11D3017D7A524DC CRC64;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang K., Iwagami S., Davies J.E.;
                                                              SERINE PROTEASE SNC19 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00561; abhydrolase; 1. PRINTS; PR00111; ABHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35896 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.1%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
325
325 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 IEVPNNOHV 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VEVPGSQHI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=2065;
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SEQUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease
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09XD79 RESULT 22 Q9XD79

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Gaps

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Q9V7M7 RESULT 23 09V7M7 ID 09

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"Genetic organization of Helicoverpa zea nuclear polyhedrosis virus in "Genetic organization of Helicoverpa zea nuclear polyhedrosis virus in the region of EcoRI U.D.L.A and Q.";
Submitted (JUN.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275264; AAG17375.1;
SEQUENCE 527 AA; 59935 MW; ElDF20478A77574C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                           Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
TYOENS A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.1%; Score 36; DB 14; Length 527; Best Local Similarity 54.5%; Pred. No. 1.3e+02; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                             STRAIN=FRIEDLIN;
Jamesrmann W., Wambutt R., Ivens A.C., Murphy L., Quail M.,
Rajandream M.A., Barrell B.G.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                               "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
Membi, ALI33436; caba62821.1; -.
Hypotherical protein.
SEQUENCE 389 AA; 42733 MW; 4C1A0CF31D0DC670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.1%; Score 36; DB 5; Length 389; Best Local Similarity 66.7%; Pred, No. 96; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09E226; CTEMBLED. 16, Created)
01-MAR-2001 (TTEMBLED. 16, Last sequence update)
01-MAR-2001 (TTEMBLED. 16, Last sequence update)
01-MAR-2001 (TTEMBLED. 16, Last annotation update)
0RF119-LIKE PROTEIN.
Helicoverpa zea nuclear polyhedrosis virus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) HYPOTHETICAL 42.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 AA.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||::||| |
107 PGARHIDVQ 115
                                                                                                                                          SEQUENCE FROM N.A.
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Q9E226
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Search completed: July 16, 2001, 16:43:37 Job time: 471 sec

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Mos Jul 16 16:58:10 2001

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	1: July 16, 2001, 16:35:41 ; search time 56.06 Seconds (without alignments) 22.710 Million cell updates/sec
	OM protein	Run On:

	VIIII 01/:77
Title:	US-09-786-648-4
Perfect score:	106
Seguence:	1 GATFQVEVPGSQHIDSQKKAI 21
Scoring table:	BLOSUM62

412676 seqs, 60623988 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

412676

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1980. /SIDS8/gcgdata/geneseq/geneseqp/AA1981 A_Geneseq_0601:* 10: Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SATOVEA	704/0155	AAW04857	AAR94939	AAW06606	AAW06607	AAW80808	AAR04163	AAP93561	AAW0660	AAW5977	AAY96652
	7	17	17	17	17	19	11	10	17	19	21
001	0 0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
106	7	106	106	106	106	106	106	106	106	106	106
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	100 O O 1	106 100.0 21 21 AAY87462	106 100.0 21 21 AAY87462 106 100.0 103 17 AAW04857	106 100.0 21 21 AAY87462 106 100.0 103 17 AAW04857 106 100.0 103 17 AAR94939	106 100.0 21 21 AAY87462 106 100.0 103 17 AAN04857 106 100.0 103 17 AAR84939 106 100.0 103 17 AAN06606	106 100.0 21 21 AAY87462 106 100.0 103 17 AAW04857 106 100.0 103 17 AAR94939 106 100.0 103 17 AAW06606 106 100.0 103 17 AAW06606	106 100.0 21 21 AAYB7462 106 100.0 103 17 AAW04857 106 100.0 103 17 AAR04939 106 100.0 103 17 AAR06606 106 100.0 103 17 AAW06607 106 100.0 103 17 AAW06607	106 100.0 21 21 AAWS7462 106 100.0 103 17 AAWS6857 106 100.0 103 17 AARS64939 106 100.0 103 17 AARS6606 106 100.0 103 17 AAWS6607 106 100.0 103 19 AAWS6808 106 100.0 118 11 AARS6163	106 100.0 21 21 AAV87462 106 100.0 103 17 AAR046857 106 100.0 103 17 AAR06606 106 100.0 103 17 AAR06606 106 100.0 103 17 AAW06607 106 100.0 103 17 AAW80808 106 100.0 118 11 AAR04163 106 100.0 124 10 AAR94163	106 100.0 21 21 AANB7462 106 100.0 103 17 AAR94935 106 100.0 103 17 AAR94939 106 100.0 103 17 AAR06606 106 100.0 103 17 AAR06607 106 100.0 103 19 AAR9808 106 100.0 118 11 AAR94361 106 100.0 124 17 AAR06605	106 100.0 21 21 AAYB7462 106 100.0 103 17 AAR94939 106 100.0 103 17 AAR96606 106 100.0 103 17 AAW66607 106 100.0 103 17 AAW6607 106 100.0 103 19 AAW86607 106 100.0 118 11 AAR9163 106 100.0 124 10 AAP93561 106 100.0 124 17 AAW96605 106 100.0 124 19 AAW96505

LTB-CTB fusion pro	LTB-CTP fusion pro	HSV-1 antiqen/heat	Sequence of sub-un	E. coli heat labil	ADP-ribosylating t	Escherichia coli v	E. coli heat-labil	Heat labile toxin	E coli verotoxin-1	Recombinant exotox	Recombinant exotox	Recombinant exotox	Recombinant exotox	Labile toxin (LT-B	C. jejuni flagelli	Plant-optimized V.	GtfB.1/CTB chimeri	B subunit of CT.	Adhesin/V.cholerae	Helicobacter pylor	Helicobacter pylor	Sequence of amino	Network polymer wh	Network polymer wh	Adhesin/CTXA2B chi	Sequence of amino.	CTP3 epitope of th	Cholera toxin B an	Residues 50-64 of	Cholera toxin B/en	Cholera toxin B su	Bovine rotavirus V
AAR50227		AAR11272	Æ	L AAY87463	5 AAR72545			L AAY68365	2 AAB66239				2 AAB73244) AAW67443				9 AAW74466	AAW80599		AAP30600	AAP50436	AAP50439		æ) AAP93498	5 AAR85125	5 AAR76748		-	L AAB15526
131 11	170 20	405 12	9	~	93 16					134 22			163 22						461 19			47 4	46 6	41 6	461 20	-	15 1(23 16		15 21	15 23
	100.0		.7						95.3	95.3	95.3	95.3	95.3	95.3	95.3	94.3	94.3	88.7	88.7				84.0	83.0	82.1	75.5	71.7	71.7	71.7	58.5	57.5	57.5
106	106	106	103	101	101	101	101	101	101	101	101	101	101	101	101	100	100	94	94	94	94	92.5	88	88	87	80	16	97	16	62	61	61
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	. 58	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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AAY87462 standard; peptide; 21 AA

AAY87462;

(first entry) 03-JUL-2000

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta 4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Vibrio cholerae. Escherichia coli

WO200014114-A1.

16-MAR-2000.

99WO-GB02970. 07-SEP-1999; 98GB-0019484, 07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1.

functional

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or may not be of Bordetella origin, can be used for the expression in Bordetella of enzymes, antigens, immunogens, allergens, enzyme inhibitors, hormones, lamphokines, immunogens, allergens, enzyme inhibitors, hormones, lamphokines, immunogens, allergens, enzyme fragments, toxins, mammalian proteins, structural proteins or receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, fha promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae, leaders used in the constructs are selected from the cholera toxin B leader (CTB-L), the pertussis toxin subunit S1 leader (S1-L) and the pertussin pertactin clader (PRN-L); and genes used in the constructs are selected from a novel synthetic cholera toxin B gene (ctb) and the hmwl and hmw2 genes of Haemophilus influenzae.
                                                                                                            Bordetella operatively linked to a heterologous gene or a non-
Bordetella leader sequence for secretion of a gene product which may
                                                                                    constructs comprising a promoter
                        Example 1; Figure 1; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT18799, AAT18800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adjuvant; immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-230602/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9612801-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arntzen CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR94939;
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                                                                                                                                                          GW-1 ganglioside receptors on host cell surfaces. Both Erx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) activity, while the B subunits (EtxB and CtxB) activity of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain through GM-1 binding. The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtxB and CtxB, exerting the same effects as normal EtxB and CtxB, such as immunomodulator or adjuvant. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea.

Therefore, the peptides may be used in the production of a composition of a composition of a composition continued alsorder and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAV87460-Y87463. Partholally being and the invention, AAV87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                           The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin; structural protein; receptor; heterologous gene; leader; promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 106; DB 21;
100.0%; Pred. No. 2.7e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW04857 standard; Protein; 103 AA.
                        Disclosure; Page 15; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic cholera toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATFQVEVPGSQHIDSQKKAI 21
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9626282-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW04857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Gaps

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Length 103; Indels

Score 106; DB 17; Pred. No. 1.7e-10; ; Mismatches 0;

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A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunishing animals
                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                     Toxin; subunit; vaccine; transgenic plant; immunogen; antigen;
                                                                           Heat labile enterotoxin B subunit (LT-B) E.coli.
                                                                                                                                                                                                                                                                                                                 Mason HS;
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 100-101; 130pp; English.
AAR94939 standard; Protein; 103 AA
                                                                                                                                                                                                                                                                                                                 Hag TA,
                                                                                                                                                                                                                                                                                        (TEXA ) UNIV TEXAS A & M SYSTEM.
                                                                                                                                                                                                                                                                          (TULA ) TULANE EDUCATIONAL FUND
                                                                                                                                                                                                                       95WO-US13376.
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Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and

Zealey GR;

Klein MH, Loosmore SM, Yacoob RK,

WPI; 1996-425088/42.

N-PSDB; AAT38038.

gene of interest

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AAW06607
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using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or optionally LT-A or CT-A.
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                  Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein,
                                                                                                                                                                                                                                                                              Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                               ;
0
                                                                                                             Length 103;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                   /label= substitution
/note= "wild-type Thr replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "wild-type Ala replaced by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "wild-type His replaced by Asn"
                                                                                                           100.0%; Score 106; DB 17;
100.0%; Pred. No. 1.7e-10;
ive 0; Mismatches 0;

    Vibrio cholerae.
    Enterotoxigenic Escherichia Coli.

                                                                                                                                                                                                                                                                                                                                                                                                                               /label- substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= substitution
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                     AAW06606 standard; Protein; 103 AA.
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                                                                                                                                                  21
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                                                                                                                                                                                                                                                             (first entry)
                                                                                                                    Local Similarity 100. nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                               103 AA;
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Misc-difference
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                                                                                                                                                                                                                                                            06-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                   Chimeric
Chimeric
                                                                                Sequence
                                                                                                            Query Match
                                                                                                                                                                                                                                       AAW06606
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Matches
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Gaps
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certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to
                                                                                                                                           protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see AAW06605).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 1..25
Misc-difference 1..25
/label= substitution
/note= "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 106; DB 17;
100.0%; Pred. No. 1.7e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic Escherichia Coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GATFQVEVPGSQHIDSQKKAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vomiting; food poisoning.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-506108/50.
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                                                                                                                                                                                                                                                                                                                                                                                            103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT43577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW06607;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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the possibility for commercial mucosal adjuvants for use in since these are more effective and safer than vaccines

administered subcutaneously

enables

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AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea can vomiting, in humans and animals.

C and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a confined mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin B subunit; nontoxic subunit; adjuvant; coadministration; antigen; bird; animal; mucosal; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of the cholera toxin B subunit used in the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as an mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered with an antigen to birds and mammals
                                                                                                                                                                                                                                                                                                                                        ;
;
                                                                                                                                                                                                                                                                                                       Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                       100.0%; Score 106; DB 17; 100.0%; Pred. No. 1.7e-10;
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                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW80808 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1B; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takeda Y,
                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                          1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US06725.
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                                                                                                                                                                                                                                                                                                                                          21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCGHEE J R.
TAKEDA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-594478/50.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YAMA/) YAMAMOTO S.
                                                                                                                                                                                                                                                       103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KIYO/) KIYONO H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09845324-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1998;
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                                                                                                                                                                                                                        AAW06605).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kiyono H,
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW80808;
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                                                                                                                                                                                                                                                                       cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                                                                          Gaps
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                                                                  Length 103;
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larity 100.0%; Pred. No. 2e-10;
Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hybrid protein, useful in vaccines -
contains cholera toxin b subunit and heterologous IgA active
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                               1..11
/*label= signal peptide
/*note= absent from mature protein
                                                                  Score 106; DB 19;
Pred. No. 1.7e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYLI-) L'UNIVERSITE DE L'ETAT A LIEGE.
                                                                                                                                                                                                                                                                                                             Location/Qualiflers
                                                                                                                                                                                                                                                                                                                           18..18
/*label= His or Tyr
                                                                                                                                                                                    AAR04163 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martial J;
                                                                  Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                                                                 65
                                                                                                             1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                        45 gatfqvevpgsqhidsqkkai
                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                   Cholera Toxin B-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-132273/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic sequence.
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les 21; Conserv
                                       103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AA;
                                                                                                                                                                                                                                                                                                                      misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L'Hoir C,
                                                                                                                                                                                                                                                                                           synthetic
                                                                                                                                                                                                          AAR04163;
                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence
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                                                                                                                                                                                                                                                                                                                                              region
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Matches
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AAP93561;

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RESULT

Peptide Protein

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AAW06605 is the full (including the signal peptide) length cholera toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amino acids (aa) of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see AAW06605 and AAW06607. The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic lilness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.
                 Cholera toxin B subunit, used for hybrid immunogenic toxin production.
                                                Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterforxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                     1..21
/label= sig_peptide
22..124
/label= mat_protein
                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW59770 standard; Protein; 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-506108/50
                                                                                                                                                                                                                                                                                                                                                                                                                                            HOLMGREN J.
LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT43575
                                                                                                                                              Vibrio cholerae
                                                                                                                                                                                                                                                                                              WO9634893-A1
                                                                                                                                                                                                                                                                                                                                                                     02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                  07-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            (LEBE/) 1
                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                    Peptide
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ID AAW5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In the patent, the DNA encoding LT-B is expressed as part of a fusion protein with an epitope of a malaria parasite, eg Region I or Region II or a repeat region of circumsporozoite protein antigen (CS) (AAP93560) from Plasmodium bergion of circumsporozoite protein antigen (CS) (AAP93560) attenuated Salmonella enteriditis under the left promoter control of lambda. Such bacteria can multiply in the host without causing disease disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be multivalent.
                                                                                                                                                                                                B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malaria; circumsporozoite protein; fusion protein; live recombinant vaccine;
                                                                                                                                                             B subunit of the heat-labile enterotoxin (LT-B) derived from E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising attenuated entero-invasive bacterium contg. DNA encoding epitope of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 106; DB 10;
Pred. No. 2.2e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hockmeyer WT;
                                                                                                                                                                                                                                                                                                                                            /note="Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Live recombinant vaccine for malaria
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /note="Mature LT-B"
                                                AAP93561 standard; protein; 124 AA.
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100.0%;
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Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-114399/15.
                                                                                                                                                                                                                                      Salmonella; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA;
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                                                                                                                                                                                                                                                                             coli.
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                                                                                                                         06-JUN-1990
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                                                                                                                                                                                                                                                                           Escherichia
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Brey RN,

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Length 124; Indels

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AAW06605;

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RESULT

AAW06605

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New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                     (BOYC-) BOYCE THOMPSON INST PLANT RES
                                           99WO-US30747
                                                                 98US-0113507
                                                                                                                                Mason HS, Arntzen CJ;
                                                                                                 (MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                   WPI; 2000-442653/38.
N-PSDB; AAA51156.
                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AA;
  WO200037609-A2
                                                                 22-DEC-1998;
                                           22-DEC-1999;
                      29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
Beta-subunit of heat labile enterotoxin; LTB; fusion protein; vaccine; immunogen; antigen; inhibin; fertility; follicle stimulating hormone; FSH; sperm; ova; immune response.
                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (LTB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antigenic peptide is an inhibin fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducing an immune response against the antigenic peptide. Vaccines are particularly administered orally, e.g. fusion protein is expressed in edible plants or animals.
                                                                                                                                                                                                                         New nucleic acid encoding fusion of antigenic peptide and enterotoxin sub-unit - useful as vaccinating immunogen, particularly for increasing animal fertility by inducing antibodies against inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant-optimized E. coli heat labile toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 106; DB 19;
100.0%; Pred. No. 2.2e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..21
/label- signal_peptide
22..124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96652 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                  Disclosure; Fig 9; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                96US-0747410.
                                                                                                                                                    (UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                                          Bagdasarian M, Ireland J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adjuvant; anti-bacterial
                                                                                                                                                                                               WPI; 1998-297947/26.
                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA;
                                                                                                                                                                                                         N-PSDB; AAV41573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
Synthetic.
                                           Escherichia coli
                                                               WO9821344-A1
                                                                                                                                12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2000
                                                                                     22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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This synthetic Escherichia coli heat-labile toxin (LT) B subunit (LT-B) is encoded by a plant-codon optimized cDNA. The cDNA sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. The second codon is changed from AAT encoding Asn to GTG encoding Val, in order to create a NcoI restriction site at the 5' end. Novel polynuclectides encode a mutant LT-A polypeptide or a wutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide or a which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the polynucleotides in transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic contractment against E. coli or V. cholerae. The mutant polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 106; DB 21;
100.0%; Pred. No. 2.2e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label-first AA of mature LTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23..24
/label-AAs encoded by linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..21
/label=LTB leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholera toxin; diarrhoea; enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR04825 standard; protein; 131 AA.
Claim 4; Fig 5A-B; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 gatfqvevpgsqhidsqkkai 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholreae serogroup 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTB-CTB fusion protein.
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Peptide

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Self-tolerance; fusion protein; immune response; LTB; CTP; hCG; cancer; labile toxin subunit B; carboxy terminal peptide; prophylaxis; fertility; human chorionic gonadotrophin; LTB-CTP.
                                                                                                                                                                                                                                                                                                                                                                                                       The surface M protein of Group A streptococi is the major virulence factor and protective antigen of these organisms. However, there are a tremendous number of M protein serotypes. The invention provides recombinant M protein antigens comprising a gene encoding a carrier protein and an NH2 or COOH terminal M protein fragment carrying one or more epitcopes. The carrier may be the B subunit of E.coli labile toxin (IT-B). The carrier and the antigen may be linked by a linker, eg AAR50226. The LT-B-M24 fusion gene of the example was expressed using E.coli. The M24 component constists of a pair of synthetic inmunised with the IT-B-W34 developed type-specific bacteriocidal antibodies against type 24 streptococci.
                                                                                                                                                                                                                                                                                                       New recombinant hybrid streptococcal M protein antigen(s) - which ellcit opsonic antibodies without eliciting cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ced. No. 2.4e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "LTB protein"
125..133
/note= "linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                          antibodies to mammalian heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "LTB protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW94082 standard; Protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08; FL
                                                                                                                                                                                     (UYTE-) UNIV TENNESSEE RES CORP
                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
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                                                                                                                                                   92US-0945860
                                                                                                                   93WO-US08704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 gatfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTB-CTP fusion protein.
                                                                                                                                                                                                                                                       WPI; 1994-118162/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                          N-PSDB; AAQ45159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                   16-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1999
                                                 WO9406465-A.
                                                                                 31-MAR-1994
                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW94082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                       Dale JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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Matches
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   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression of binding sub-unit protein of cholera toxin - using foreign promoter with no V cholera DNA between promoter and ribosome binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is produced by genetically fusing the leader sequence for E.coli heat-labile enterotoxin subunit (LTB) by its 3' SacI end to the 5' Ndel end of the cholera toxin subunit (CTB) via a syntheter linker. This allows the use of a strategically placed EcoRI site just upstream of the RBS on the LTB gene for the insertion of a strong tac promoter for the expression of CTB. The protein can be used as vaccines, cholera and receptor-blocking agents for prophylaxis of cholera and E.coli diarrhoes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B subunit; labile toxin; M protein; fusion protein; antigen; Group A streptococci; rheumatic fever; pharyngitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                 'label-cleavage to release mature CTB
                                                                                                     25..26
Alabel=cleavage to release mature CTB
25..28
/label-part of CTB leader sequence
29..131
                                                                                                                                                                                                                                                       /label=D = N in classical 569B CTB
                                                                                                                                                                                                                                                                                         /label=D = N in classical 569 CTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 106; DB 11;
Pred. No. 2.3e-10;
; Mismatches 0;
                                                                                                                                                                                   label=T = I in El Tor CTB
                                                                                                                                                                                                                     /label=G - S in El Tor CTB
                                                                                                                                                   abel-H - Y in El Tor CTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of LT-B-M24 hybrid molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR50227 standard; Protein; 138 AA.
                                                 'label=mature CTB
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Best Local Similarity 100.0%;
Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                          89EP-0850295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            89NO-0003702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; ; p; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanches C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-149724/20.
P-PSDB; AAR04825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HOLM/) HOLMGREN J.
                                                                                                                                 Misc-difference 46
                                                                                                                                                                 Misc-difference 75
                                                                                                                                                                                                                                     Misc-difference 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 AA;
                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                     Misc-difference
                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-1989;
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15-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmgren J,
                                                                                                                                                                                                                                                                                                                                                         16-MAY-1990
                                                                                                                                                                                                                                                                                                                       EP368819-A.
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RESULT 13 AAR50227

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Gaps

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Protein

Rock EP;

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A desired truncated gene is cut out from a plasmid in which the gD or gB gene (opt. lacking a transmembrane domain, full details not given for this sequence) of HSV-1 strain Miyama has been cloned. It can also be chemically synthesised.

An appropriated linker is added to it as needed, followed by construction of a fused gene in which an LTB gene is linked to the 3' end. The resulting fused protein gene is ligated downstream from
                                                                                                                                                                                                                                                                                                                                                                                                        a promoter in an expression vector.
The product is effecient for targetting to masal mucosa tissues compared to unfused proteins. It can induce an immune response. The protein is useful as immunogen in vaccines for therapeutic and preventive use, or for treatment of viral, pathogenic protezoan or bacterial infections.
                                                                                                                                                                    Fused protein used to treat viral and pathogenic bacterial infections - contg. heat labile enterotoxin B sub-unit and herpes-simplex virus antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 106; DB 12;
100.0%; Pred. No. 8.6e-10;
ive 0; Mismatches 0;
                                                                          Yamamoto T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; cholera; heat-labile E.coli toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                              Disclosure; Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50340 standard; protein; 103 AA.
                                                                            Mayumi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50..64
/note= "claimed"
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                                     (TAKE ) TAKEDA CHEMICAL IND KK.
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89JP-0233728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84DE-3430894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83IL-0069558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
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45..64
                                                                          Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                             WPI; 1991-088294/13.
N-PSDB; AAQ11073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholera
08-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-1984;
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                                                                          Fujisawa Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE3430894-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to breaking self-tolerance against self protein in a mammal that comprises administering a fusion protein for eliciting an immune response, the fusion protein comprising pentamers of Escherichia coll labile toxin subunit B (LTB) and carboxy terminal peptide (CTP) of human chorionic gonadotrophin (hGG). The fusion protein can also be used in a method of inducing antibody against protein in a mammal. The methods can be used to break self-tolerance and can produce antibodies to hGG. They can be used for prophylaxis and therapy, e.g. in the treatment of cancers or control of mammalian fertility. The method circumvents the chemical variability, complex preparation, side effects, and expense of other vaccines to break self tolerance that rely on passive immunisation, chemical conjugation with additional adjuvant, or lymphokine supplementation. The present sequence represents a LTB-CTP fusion
                                                                                                                                                                                                                                                                                                                                                          Breaking self-tolerance against self protein - using fusion proteins producing pentamers of Escherichia coli labile toxin subunit B and human chorionic gonadotrophin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSV-1 antigen/heat-labile enterotoxin B subunit fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes Simplex Virus-1; HSV-1; heat-labile enterotoxin;
subunit B; LTB; vaccine; nasal mucosa tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 106; DB 20;
100.0%; Pred. No. 3.1e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSV-1 strain Miyama, Escherichia coli
                 /note= "CTP protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 4A-B; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR11272 standard; Protein; 405 AA.
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                                                                                                                               97US-0944982
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97US-0944982
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134..149
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 AA
                                                                                                                                                                                                                          (ROCK/) ROCK E P.
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX06654.
                                                                                                                                 07-JUN-1997;
                                                                                                                                                                    07-JUN-1995;
07-OCT-1997;
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                                                      US5869057 - A.
                                                                                           09-FEB-1999
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Best_Loca Matches

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Length 405;

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31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1995.
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                                                                                                                                                                                                                                                                                          AAR72545;
                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from wibino cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (APP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the
                                                                                                The inventors claim vaccines against cholera and heat-labile E.coli toxin contg. cholera toxin fragment coupled to carrier. The toxin is esp. the fragments defined in FT, above.
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Heat labile enterotoxin subunit B; EtxB;
beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Derivatives of Escherichia coli heat labile enterotoxins useful a immunomodulators and for treating diarrhea and which do not bind
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                                                                                                                                                                                                                                                                                                                                                                     E. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5.
                                            Vaccines against cholera and heat-labile E. coli toxin - contg.
                                                                                                                                                                               Length 103;
                                                                                                                                                                                                   0; Indels
                                                                                                                                                                             Score 103; DB 6;
Pred. No. 5.6e-10;
                                                                                                                                                                                                   Mismatches
                                                       cholera toxin fragment coupled to carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                    AAY87463 standard; peptide; 21 AA.
                                                                                                                                                                                                                                             65
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                                                                                                                                                                             97.28;
95.28;
                                                                            Example; Fig 1; 24pp; German.
Arnon R, Jacob CO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-GB02970
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                                                                                                                                                                                                                                    1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycolipid receptor GM-1 -
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                            Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams NA, Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-256943/22.
                      WPI; 1985-069683/12.
                                                                                                                                             103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200014114-A1.
                                                                                                                                                                                                                                                                                                                                                03-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-2000
                                                                                                                                               Sequence
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Sela M,
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                                                                                                                                                                                                                                                                                         AAY87463
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beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAX87460-X87463 represent preferred peptides of the invention, AAX87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify stres which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella pertussis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hazes B, Klein MH, Loosmore S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 21;
Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP-ribosylating toxin (verotoxin-1 B-subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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95.2%;
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Oomen R, Read RJ, Stein PE;
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94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                      AA;
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AAW95226

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A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises:

(1) identification of at least one amino acid (aa) residue of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein replacing a nucleotide sequence encoding at least one (aa) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties.

Structure, Modifying the holotoxin, alters its biological properties.

By analysing the 3-dimensional crystalline structure of the pertussis holotoxin (an) which affect biological properties of the pertussis holotoxin (an) which affect biological properties of the pertussis holotoxin (an) which affect biological properties of the pertussis holotoxin (an) which affect biological properties of the pertussis holotoxin (an) which affect biological properties of the characteristic properties of the control of the pertussis holotoxin (an) which affect biological properties of the control of the pertussis holotoxin (an) which affect biological properties of the control of the pertussis holotoxin (an) which affect biological properties of the control of the pertussis holotoxin (an) which affect biological properties of the control of the pertussis holotoxin (an) which affect biological properties of the control of the pertussis holotoxin (an) which affect biological properties of the control of the pertussis holotoxin (an) which affect biological properties of the control of the pertussis the control of the control of the contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin B-subunit peptide used in the exemplification of the present
                                                                ö
            Length 93;
                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New method for producing modified pertussis holotoxin
            Score 101; DB 16;
Pred. No. 1.1e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli verotoxin-1 B-subunit.
                                                                                                                                                                                                                                                                                   AAY41816 standard; peptide; 93 AA.
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                                                                                                                                     1 GATFQVEVPGSQHIDSQKKAI 21
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93US-0110947.
94US-0251121.
            95.3%;
95.2%;
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Query Match
Best Local Similarity 95.2'
Matches 20; Conservative
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Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-579908/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-1999
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Hazes B,
                                                                                                                                                                                                                                                                                                                                    AAY41816;
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The invention relates to methods of preparing a pertussis holotoxin (PT)
having a modified biological activity. One method comprises identifying
at least 1 site in a PT that interactis with a molecule that is capable of
comming a complex with the holotoxin and which molecule is an effector
considerable which is an adenine nucleotide and which site contributes to
considerable which is an adenine nucleotide and which site contributes to
considerable is an effector
control interacting site(s) are identified by analysing the three dimensional
structure of crystalline PT, determined by X-ray crystallogaphy. The
identified interacting site(s) are modified to alter toxicity, cell
control interacting site(s) are modified to alter toxicity, cell
binding or enzyme activity of the PT. The methods can be used to alter a
biological activity such as toxicity, enzymatic activity, mitogenicity,
cell binding and adjuvanticity of the PT. The three-dimensional structure
of PT have functional and/or structural resemblance to other bacterial
conference in the conference of the proper conference in the property of the property conference in the property conference i
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                                                                                                                                                                                      Pertussis holotoxin; PT; modified; effector; toxicity; cell binding;
                                                                                                                                                                                                                 enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography;
structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loosmore
                                                                                                                                          E. coli heat-labile toxin (LT) beta-subunit sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 101; DB 20;
Pred. No. 1.1e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď,
    AA.
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Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 5; 40pp; English.
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AAW95226 standard; peptide; 93
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94US-0251121.
                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cockle SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GD, Cockle
Read RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-105104/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1994;
                                                                                           16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                         US5856122-A.
                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Armstrong
Oomen RP,
                                              AAW95226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 20
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                        Op
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Gaps

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Indels

Length 93;

Score 101; DB 20; Pred. No. 1.1e-09; 0; Mismatches 1;

95.3%; 95.2%;

Conservative

20;

Best Local Similarity

Query Match Matches

AAY68365;

AAY68365

RESULT

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The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of minunoprotective analogues of pertussis toxin is the cause of whooping cough following infection
                                                                                                            Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oomen RP, Loosmore S, Klein MH, Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 22;
Pred. No. 1.1e-09;
                                                                           E coli verotoxin-1 B subunit SEQ ID NO: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant exotoxin protein variant LTBpL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB73241 standard; Protein; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 5; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                 93US-0110947,
94US-0251121,
                                                                                                                                                                                                                                                                                                        98US-0082514
                                                                                                                                                                                                                                                                                                                                             94US-0292968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                   03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                  islet-activating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cockle SA,
Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-122260/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                          toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                             US6168928-B1
                                                                                                                                                                                                                                                                                                        21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                             22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                 24-AUG-1993;
                                                                                                                                                                                                                                                                  02-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-2001
                                                                                                              Pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB73241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
AAB66239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB73241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a crystalline form of isolated pertuasis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. Ay68340 to AAY68385 represent peptides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Armstrong GD;
                                                                                                                                                                                                                         Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crystalline form of isolated pertussis holotoxin useful in studying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB 21;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins which have functional resemblance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                     Heat labile toxin B subunit SEQ ID NO:26
                                                                     AAY68365 standard; Peptide; 93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cockle SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 5; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0467976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0110947
94US-0251121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0292968
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                                                                                                                                                  17-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 95.3
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-136703/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 AA;
                                                                                                                                                                                                                                                                                                                        Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                      immunogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                             US6018022-A
                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Read RJ,
Hazes B,
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(UYAL-)

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Gaps

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Indels

Unidentified

AAB66239 standard; Protein; 93 AA.

AAB66239

e X

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Sequence

Length 93;

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The present invention relates to recombinant exotoxin protein variants, affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition comprising the protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia cell was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin
                                         Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 22;
Pred. No. 1.8e-09;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant exotoxin protein variant LTB-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB73243 standard; Protein; 155 AA.
                                                                                                                            Example 1; Fig 10; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 11; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.3%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0149294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-2000; 2000WO-US22715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 getfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.3
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-211103/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA;
N-PSDB; AAF75713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF75714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200111960-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welter LM;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (ADARD) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition comprising the protein variant.
                                                                                                                                                                                                                                                                                                                Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 22; Length 134;
Pred. No. 1.7e-09;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant exotoxin protein variant LTBpLh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73242 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 9; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.3%;
95.2%;
                                                                                   18-AUG-2000; 2000WO-US22715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-2000; 2000WO-US22715.
                                                                                                                            99US-0149294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                     WPI; 2001-211103/21.
                                                                                                                                                                      (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-211103/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 AA;
WO200111960-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200111960-A1
                                                                                                                            18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 20; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2001.
                                         22-FEB-2001
                                                                                                                                                                                                              Welter LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB73242;
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RESULT 24 AAB73242

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Gaps

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(bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an artigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition comprising the protein variant.
8888888
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155 AA; Seguence

ó; 0; Gaps Query Match 95.3%; Score 101; DB 22; Length 155; Best Local Similarity 95.2%; Pred. No. 2e-09; Matches 20; Conservative 0; Mismatches 1; Indels C

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Search completed: July 16, 2001, 16:35:41 Job time: 205 sec

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US-08-952-337-5

Sequence 5, Application US/08952337

Patent 'No. 6019973

'GENERAL INFORMATION'

APPLICANT: Lebens, Michael R.

TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE

TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE

TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN TOXIN B SUBUNITS

FILE REFERENCE: 3846/0D758

CURRENT FILING DATE: 1998-01-05

EARLIER APPLICATION NUMBER: PCT/SE96/00570

EARLIER APPLICATION NUMBER: SE 9501682-0

EARLIER PILING DATE: 1995-05-05

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 5

LENGTH: LOS

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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN B SUBUNITS
FILE REFERENCE: 3846/OD758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1995-05-05
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US-08-961-810-133
US-08-352-902D-133
US-07-956-700B-94
US-08-476-537-94
US-08-476-537-94
US-08-476-537-94
US-08-402-395-34
US-09-025-580-36
US-09-025-580-36
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US-08-469-803-11
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US-08-952-337-6
Sequence 6, Application US/08952337
Patent No. 6019973
GENERAL INFORMATION:
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Best Local Similarity
Matches 21; Conserv
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                TYPE: PRT
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Sequence 12, Appl
Patent No. 5223610
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Sequence 2, A
Sequence 2, A
Sequence 23,
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-947-526-2

US-09-013-047-2

US-09-121-852-21

US-08-922-337-1

US-08-922-337-1

US-08-922-337-2

US-08-922-337-2

US-08-922-337-2

US-08-922-337-2

US-08-747-410-2

US-08-747-914-26

US-08-467-536-26

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US-08-467-536-26

US-08-467-536-26

US-08-487-916-26

US-08-823-10-8

US-08-823-10-8

US-08-823-10-8

US-08-878-989-2

US-08-878-989-2

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US-09-059-461-2
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Sequence 2, Application US/08894526 Patent No. 5942418
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REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
INFORMATION FOR SEQ. ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09013047
Patent No. 5998168
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                     APPLICANT: Loosmore, Sheena M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-894-526-2
                                                                                                                                 GENERAL INFORMATION:
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US-09-013-047-2
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Patent No. 593274
GENERAL INFORMATION:
APPLICANT: LOGSMORE, Sheena M.
APPLICANT: Zealey, Gavin R.
APPLICANT: Yacoob, Reza K.
APPLICANT: ALea, Michel H.
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE Sim & MCBurney
STREET: 330 University Avenue, Suite 701
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                                                                                                                                                                                          100.0%; Score 106; DB 3; Length 102; 100.0%; Pred. No. 2e-11;
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                                                                                                                                                                                                                                     0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PAETENT Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/393,334
ATLING DATE: 23-FEB-1995
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 106; DB 2;
100.0%; Pred. No. 2.1e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
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TELEPHONE: 416-595-1155
TELEFAX: 416-595-1163
                                                                                                                                                                                                                                                                            1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                      44 GATFQVEVPGSQHIDSQKKAI 64
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                       ; ORGANISM: Escherichia coli
US-08-952-337-6
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Best Local Similarity 100.0
Matches 21; Conservative
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Matches 21; Conservi
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                                                                LENGTH: 102
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                                                                                      TYPE: PRT
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APPLICANT: Yacoob, Reza K
APPLICANT: Zealey, Gavin R
APPLICANT: Zealey, Gavin R
APPLICANT: Zealey, Gavin R
APPLICANT: Zealey, Gavin R
APPLICANT: Rein, Michal H
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toront
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                       STATE: Ontario
COUNTRY: Canada
ZIP: M5G 119.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/894,526
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
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Pred. No. 2.1e-11;
; Mismatches 0;
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STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ontario
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Canada

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Gaps

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ADDRESSE: Fulbright & Jaworski L.L.P.
STREET: 1301 MCKinney, Suite 5100
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,852
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 106; DB 4;
100.0%; Pred. No. 2.1e-11;
Live 0; Mismatches 0;
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Pred. No. 2.1e-11;
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael 1
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-964
TELECOMMUNICATION INFORMATION:
TELERAX: 416-595-1155
TELEX: 06-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: FOX, DAVIG L.
REGISTRATION NUMBER: 40,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P01590US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 21, Application US/09191852; Patent No. 6194560; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-374-597-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 77010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: TX
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TOPOLOGY:
US-09-191-852-21
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US-09-191-852-21
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,597
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 106; DB 2; ilarity 100.0%; Pred. No. 2.1e-11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1038-507 MIS:VG
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,171
FILING DATE: 0'-JUN-1995
PRIOR APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MI.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
PLIUR DATE: PEBRUARY 23, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Loosmore, Sheena M.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Lealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression O
TITLE OF INVENTION: Genetically
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBLINEY
ADDRESSEE: SIM & MCBLINEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09374597
Patent No. 6140082
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 103 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-013-047-2
                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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Best Local Similarity
Matches 21; Conserv
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Sequence 2, Application US/08952337

Patent No. 6019973

GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
CURRENT SPERENCE: 3846,0078

CURRENT APPLICANTON NUMBER: US/08/952,337

CURRENT APPLICANTON NUMBER: PCT/SE96/00570

EARLIER APPLICANTON NUMBER: PCT/SE96/00570

EARLIER FILING DATE: 1996-05-05

EARLIER FILING DATE: 1996-05-05

SOFTWARE: FALLING DATE: 1995-05-05

SOFTWARE: FALLING DATE: 1995-05-05
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STREET: 3100 No. 5993820west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 123;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106; DB 3;
Pred. No. 2.6e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                   Score 106; DB 3;
Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                     Mismatches
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APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
TITLE OF INVENTION: CHIMERIC LTB VACCINES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 123
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100.0%; Prf
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                                                                                                                                                                                                                                                                                Ouery Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     65 GATFQVEVPGSQHIDSQKKAI 85
                                                                                                                                                                                                                                                                                                                                                                                       1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Eschcerichia coli
US-08-952-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                            ; ORGANISM: Vibrio cholerae US-08-952-337-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-952-337-2
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US-08-747-410-2
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                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                 Sequence 21, Application PC/TUS9513376
GENERAL INFORMATION:
APPLICANT: The Texas A&M University System
APPLICANT: To Texas A&M University System
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 103;
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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: BY THE OF INVENTION: BY THE REFERENCE: 3846/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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100.0%; Pred. No. 2.1e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-CCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John WRES: 31,380
REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36170/3P
TELECHONE: 713-850-0909
TELEFAX: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/13376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08952337
Patent No. 6019973
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                                                                                    45 GATFQVEVPGSQHIDSQKKAI 65
                                                    1 GATFQVEVPGSQHIDSQKKAI 21
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 103 amino acids TYPE: amino acid
     21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                         PCT-US95-13376-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-13376-21
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Sequence 26, Application US/08467974

Setting No. 5965385

GENERAL INFORMATION:
APPLICANT: STEIN, Penelope E.
APPLICANT: OOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BA PC COMPATIBLE
COMPUTER: A POCHOMATIBLE
COMPUTER: TO POCHOMATIBLE
COMPUTER: TO PACHOLIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/467,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
95.3%; Score 101; DB 2;
Best Local Similarity 95.2%; Pred. No. 1.4e-10;
Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELEPHONE: (416, 595-1165
TELEPHONE: (416, 595-1165
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-UN-1995
FILING DATE: 22-AUG-1994
FRICH APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY,AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATFQVEVPGSQHIDSQKKAI 21
                                        24-AUG-1993
                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-08-292-968-26
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US-08-467-974-26
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APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & Modification of PERTUSSIS TOXIN STREET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 106; DB 2;
100.0%; Pred. No. 2.6e-11;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sim & McBurney
STREET: Sulte 701, 330 University Avenue
CITY: Proonto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: FastERO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,410
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRICA APPLICATION: DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11526.1-US-01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX:
TELECAX:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/292,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 GATFQVEVPGSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE: US-08-747-410-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-292-968-26
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Gaps

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Length 93;
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                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Torout
STATE: Ontatio
STATE: Ontatio
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: DatentIn Release #1.0, Version #1.25
STINGENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,976
FILING DATE: 06-UIN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                  Score 101; DB 2;
Pred. No. 1.4e-10;
0; Mismatches 1;
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Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Suite 701, 330 University Avenue CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-453 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-MUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/08467976 Patent No. 6018022
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOCSMORE, Sheena
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                  35 GETFQVEVPGSQHIDSQKKAI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.3%;
95.2%;
                                                                                                                                  Query Match 95.3%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-467-536-26
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                                                                                                                                                                                                                                                                                                       Length 93;
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APPLICANT: STEIN, Penelope E.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SOUDENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSE: Sim & MCBGI.

ADDRESSE: Sim & MCBGI.

STRET: Suite 701, 330 University Avenue
CITY: Toronto

STATE: Ontario

COUNTRY: Canada
ZIP: MSG 1R7

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/467,536
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                            Score 101; DB 2;
Pred. No. 1.4e-10;
0; Mismatches 1
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET VUMBER: 1038-454 MIS:v9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 and no acids
TYPE: and no acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-455 MIS:V9
TELECOMMNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08467536
Patent No. 5977304
                                                                                                                                                                                                                                                                                                                                                                                                                            35 GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                                                                                                                                                                                                                                                                                   1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                              95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            Query Match 95.3
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: READ, RA
APPLICANT: STEIN, P
APPLICANT: COCKLE,
APPLICANT: COMEN, R
                                                                                                                                                                                                                         linear
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US-08-467-974-26
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US-08-467-536-26
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Pred. No. 7.5e-10;
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Patent No. 5770203
GENERAL INFORMATION:
APPLICANT: BURNELE, Neal W.
APPLICANT: BASLOW, HARVEY R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/829,026A
FILING DATE: 18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Room 411, Building 005, BARC-W
CITY: Beltsville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/449,045C
24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.4
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0106
TELECOMUNICATION INFORMATION:
TELEPHONE: 301-504-5676
TELEPHONE: 301-504-5676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 GETFQVEVPGSQHIDSQKKAI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.3%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 371 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-829-026A-6
    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24
CLASSIFICATION:
                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                             COUNTRY: US ZIP: 20705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 18
US-08-449-045C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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GENERAL INFORMATION:
APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion P
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                    MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,514
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.08/292,968
FILING DATE: 24-AUG.1994
ATTORNEY/AGBNT INFORMATION:
NAME: STEWART, Michael I.
      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.3%; Score 101; DB 4; 95.2%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                US-09-082-514-26; Sequence 26, Application US/09082514 Patent No. 616928; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08829026A
Patent No. 5837825
                                                                                                                                                                                                                                                 APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, RAYMOND P.
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HARST, BALL
TITLE OF INVENTION: MODIFICATIO
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 GETFQVEVPGSQHIDSQKKAI 55
                                                                 STREET: 6th Floor, 330 Univ.
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATFQVEVPGSQHIDSQKKAI 21
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Best Local Similarity 95.2
Matches 20; Conservative
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20;
Matches
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Gaps
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                                                          APPLICANT: Burton, Frank H.; Sutcliffe, Gregor
: TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
:HORMONE PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                88.7%; Score 94; DB 6; Length 124; 90.5%; Pred. No. 3.3e-09; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: CORRESPONDENCE PAREMACEUTICALS, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                            NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,852
FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08878989
Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandman, Olga
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GAIFQVEVPSSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler, Karl G.
Lal, Preeti
Goli, Surya K.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corley, Neil C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                    :Patent No. 5223610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                  LENGTH: 124
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-878-989-2
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                                                                                                                                                                                                                                                                      SEQ ID NO:3:
      5223610-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
US-08-435-605A-12
US-08-435-605A-12
Sequence 12, Application US/08435605A
Patent No. 5874287
GENERAL INFORMATION:
APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                   88.7%; Score 94; DB 1; Length 124; 90.5%; Pred. No. 3.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:

COUNTRY: USA

ZIP: 91320-1789

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER FLADABLE FORM:

MEDIUM TYPE: Floppy disk

COMBUTER: IBA PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PROPARA:

APPLICATION NUMBER: US/08/435,605A

FILING DATE: 05-MAY-1995

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:

NAME: MAZZA: Richard J.

REGISTRATION NUMBER: 27,657

REFERENCE/DOCKET NUMBER: A-196B

INFORMATION FOR SEQ ID NO: 12:

LEMGTH: 124 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acids

TYPE: TYPE: TIPEDINESS: Single

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PROJUCTION INFORMATION

STRANDEDNESS: Single

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PROJUCTION INFORMATION

PROJUCTION INFORMATION

PROJUCTION

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                                                   NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REPERBENCE/DOCKET NUMBER: A-196C
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GAIFQVEVPSSQHIDSQKKAI 86
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FILING DATE: 06-JUL-1994 ATTORNEY/AGENT INFORMATION: NAME: Mazza, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 90.53
Matches 19; Conservative
                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-045c-4
                                                                                                                                                                                                                                           amino acid
GY: linear
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LIBRARY: TBLYNOT01

RESULT

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IMMEDIATE SOURCE:

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GENERAL INFORMATION:

APPLICANT: O'Brien, Thouthy J.

APPLICANT: O'Brien, Thouthy J.

APPLICANT: Tanimoto, Hirotosh.

TITLE OF INVENTION: Breast and Ovarian Carcinomas

TITLE OF INVENTION: Breast and Ovarian Carcinomas

TITLE OF INVENTION: Breast up Ovarian Carcinomas

CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 2

LENGTH: 855
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides
CTHER INFORMATION: 23 to 2589 of Sequence 1
Fatent No. 5972616
US-09-027-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08709784

Patent No. 6048701

CENERAL INFORMATION:
APPLICANT: The Johns Hopkins University
ITILE OF INVENTION: Antibody Detection of Mismatch Repair
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-FOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/709,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Banner & Allegretti, Ltd. 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107.57434
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,351
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
                                                                                                      Sequence 2, Application US/09027337B Patent No. 5972616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
      269 GOSINVHIPNSQKVDSQKAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4::|||:||:
367 TWNIEVPNNQHV 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Lac 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                 RESULT 23
US-09-027-337-2
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                                                                                   Length 448
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                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Gorley, Neil C.
APPLICANT: Groley, Neil C.
APPLICANT: Golly, Surya K.
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: NINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Forter Drive
CITY: Palo Alto
STRIET: OA
                                                                               48.1%; Score 51; DB 2;
50.0%; Pred. No. 0.55;
tive 2; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.1%; Score 51; DB 4 50.0%; Pred. No. 0.55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY_AGENT INFORMATION:
NAME: Billings, Lucy J J
REFERENCE/DOCKET NUMBER: 9F-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09272796 Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                        269 GQSINVHTPNSQKVDSQKAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TBLYNOT01
CLONE: 40194
                                                                                                                                                               1 GATFQVEVPGSQHIDSQKKA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.00
Matches 10; Conservative
                                                                                                    Best_Local Similarity 50.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
; CLONE: 40194
US-08-878-989-2
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                                                                                                                                                                                                                                                               RESULT 22
US-09-272-796-2
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Gaps

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us-uv-zuy-zul-zy

patent No. 5922855

generae 23 Application US/08209521

patent No. 5922855

general zuy-zur-zuy

APPLICANT: Liskay, Robert M.

APPLICANT: Bronner, C. Eric

APPLICANT: Blonner, Rechard D.

TITLE OF INVENTION: MAMMALIAN DHASI

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack & ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack & STREET: 520

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heuser

STREET: Oregon

COMPUTER: IBM PC Compeatible

COMPUTER: IBM PC Compeatible

COMPUTER: IBM PC Compeatible

COMPUTER: IBM PC Compeatible

ORFATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/209,521

FILING DATE: 08-MAR-1994

CLASSIECATION UNMBER: 01508

TELEPHONE: (503) 224-6655

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 862 amino acids

TTELERAX: (503) 224-6655

INFORMATION CONTENTION:

MCLECHIEF TATOR

TTELERAX: (503) 225-6679

INFORMATION CONTENTION:

TELEPHONE: (503) 225-6679

INFORMATION CONTENTION:

MCLECHIEF TATOR

TELEPHONE: (503) 225-6679

INFORMATION CONTENTION:

MCLECHIEF TATOR

MCLECHIEF TATOR

TELEPHONE: (503) 225-6679

TELERAX: (503) 225-6679

TTELERAX: (503) 225-6679
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                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                        38.2%; Score 40.5; D
75.0%; Pred. No. 85;
tive 2; Mismatches
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                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-709-784-2
LENGTH: 856 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-209-521-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GSQ-HIDSQKKA 20
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US-08-209-521-23
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10 GSQ-HIDSQKKA 20

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version 4.5
- 2000 Compugen Ltd.
  GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

July 16, 2001, 16:37:01; Search time 34.9 Seconds (without alignments) 45.836 Million cell updates/sec Run on:

1 GATFQVEVPGSQHIDSQKKAI 21 US-09-786-648-4 106 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heat-labile entero	cholera enterotoxi	RAD23 protein homo	hypothetical prote	hypothetical prote	conserved hypothet		hypothetical prote		ß	queuine tRNA-ribos	kinesin heavy chai	chorismate synthas	hypothetical prote	chitinase (EC 3.2.	stress-activated p	inner membrane pro	probable carnitine	4-aminobutyrate tr	alpha-dextrin endo	conserved hypothet	ubiquitin / riboso	`	ubiquitin 18 - sli	(C)		polyubiquitin 5 (c		ě
SUMMARIES	OI	QLECB	XVVCB	T04150	T19866	C86400	D81715	C96580	A86457	S76110	Н69231	T46898	149189	S17246	F83962	JG0178	JC5694	G81692	T49574	JC4022	S11823	F81109	UQDOR	UQDOR7	D34080	B27806	C34080	B34080	A27806	366056
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	Query Match Length	124	124	392	374	574	374	91				399	439	376	216	299	427	787	864	200	1090	91	128	154	228	229	380	380	381	386
	Query Match	5.3	4.3	5.3	3.4	3.4	2.0	1.5	1.5	1.5	9.0	9.0	9.0	0.1	9.6	9.6	9.6	9.6	9.6	9.5	9.5	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7
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	Result No.		7	3	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

polyubiquitin 7 (c hypothetical prote hypothetical prote	mutt protein homol hypothetical prote hypothetical prote	hypothetical prote protein F20B17.2 [hypothetical prote gibberellin 20-oxi hypothetical prote	thiosulfate sulfur thiosulfate sulfur hypothetical prote	hypothetical prote RNA binding protei
A34080 T01770 T20566	S47598 G69903 T32894	T34767 C96827	T24938 T01751 T04861	T52658 T01034 T16225	T16655 T39064
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ALIGNMENTS

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		chain
		enterotoxin
1	•	·labile

cursor - Escherichia coli heat-

C;Species: Escherichia coli C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999 C;Accession: A01820; B26946; I41194; I41287; I67644; A61475

R;Dallas, W.S.; Falkow, S. Nature 288, 499-501, 1980 A;Title: Amino acid sequence homology between cholera toxin and Escherichia coli heat A;Reference number: A01820; MUID:81074965

A; Accession: A01820

A; Molecule type: mRNA A; Residues: 1-124 <DAL> R; Yamamoto, T.; Gojobori, T.; Yokota, T. A; Tetriol. 169, 1352-1357, 1987 A; Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichi A; Reference number: A26946; MUID:87137303 A; Accession: B26946

A; Wolecule type: DNA A; Residues: 1-27, KE, 29-63, KK', 65-124 < YAM> A; Cross-references: EMBL: M.5363; NID: 9148335; PIDN: AAA24792.1; PID: 9148336 A; Cross-references: EMBL: W.S. R; Leong, J.; Vinal, A.C.; Dallas, W.S. Infect. Immun. 48, 73-77, 1985 A; Title: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons A; Reference number: 141194; MUID: 85156481 A; Accession: 141194

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-5, Fr, 7-17, C', 19-24, S', 26-27, E', 29-33, H', 35-63, K', 65-66, A', 68-122 A; Cass-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831 A; Experimental source: plasmid ENT-R PCG86 R; Ibrahimi, I.; Gentz, R. J. Biol. Chem. 262, 10189-10194, 1987 A; Title: A functional interaction between the signal peptide and the translation appa

A; Reference number: 141287; MUID:87280041 A; Accession: 141287 ticulum.

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-22 <RE2>

A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
FEMS Microbiol. Lett. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic A;Reference number: 153542; MUID:93252225

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1, (°, 19, Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 <R
A;Residues: 1-1, (°, 19, Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 <R
A;Residues: 1-1, (C', 19, Y', 21-34, 'S', 101-3408994; PIDN:AACG0441.1; PID:g408996
B;Tsujl, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.;
Microb. Pathog. 2, 381-390, 1987

```
A; Molecule type: protein
A; Experimental source: biotype Inaba 569B
A; Note: Asn-65 was partially deaminated to Asp
C; Commer: The authors translated the codon TCA for residue 33 as Tyr.
C; Genetics:
A; Gene: VC1456
A; Map position:
C; Genetics:
A; Gene: VC1456
A; Map position:
C; Complex: the cholera enterotoxin molecule contains three kinds of chains; an alpha ciate noncovalently with the subunit B, an aggregate of five beta chains
C; Complex: the cholera enterotoxin peta chain
C; Function:
A; Description: involved in binding of the toxin to cell membranes
C; Superfamily: cholera enterotoxin beta chain
C; Keywords: enterotoxin; toxin
C; Keywords: enterotoxin; toxin
C; Keywords: enterotoxin; toxin
C; Keywords: enterotoxin chain B #status predicted <MAT>
F; 22-124/Product: cholera enterotoxin chain B #status predicted <MAT>
E; 30-107/Disulfide bonds: #status experimental
Biochim. Biophys. Acta 1090, 139-141, 1991
A;Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A;Reference number: S17665; MUID:91355224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 22-38, H', 40-67, T', 69, E', 71, OS', 74-75, VE', 78-86, O', 88-99, O', 101-103
B; Takao, T.; Watanabe, H.; Shimonishi, Y.
B; Takao, T.; Watenabe, H.; Shimonishi, Y.
Biochem. 146, 503-508, 1985
A; Title: Facile identification of protein sequences by mass spectrometry.
A; Reference number: A21910; MUID: 85126976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 22-38, 'H', 40-41 < MAQ>
R; Residues: 22-38, 'H', 40-41 < MAQ>
R; Residues: 22-38, 'J.; Swartz, D.J.; Pearson, G.D.N.; Harford, N.; Groyne, F.; de Wilde, Nature 306, 551-557, 1983
A; Reference number: A93320; MUID: 84068199
A; Recession: A05130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 22-38, "H', 40-42, "N', 44-67, "T', 69, "E', 71-90, "N', 92-124 <LAI>
A; Residues: 22-38, "H', 40-42, "N', 44-67, "T', 69, "E', 71-90, "N', 92-124 <LAI>
A; Note: the difference at residue 70 may be due to deamidation during preparation
B; Nakashima, Y: Naplorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
A; Title: Primary structure of the B subunit of cholera enterotoxin.
A; Reference number: A38034, MUID:77026365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Determination of the primary structure of cholera toxin B subunit. A;Reference number: A38033; MUID:78005536
                                                                                                                                                                                                                A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-38, YH', 40-67, 'T', 69-124 CDA2> A; Cross-references: EMEL:X56785; NID:948888; PIDN:CAA41591.1; PID:948890 R; Ma, Q.J.; Liu, C.X.; Xiong, L.S.; Yu, X.Q. Sci. sin. B Chem. Biol. Agric. Med. Earth Sci. 34, 274-280, 1991 A; Title: B subunit of cholera toxin produced in Escherichia coli. A; Reference number: PC1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Molecule type: DNA
A. Residues: 1-32, 'S', 34-74, 'S', 76-124 < MEK>
A. Residues: 1-32, 'S', 34-74, 'S', 76-124 < MEK>
A. Cross references: GB. X00171; NID: 948347; PIDN: CAA24996.1; PID: 9758351
A. Kurosky, A.; Markl, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A. Tille: Covalent structure of the beta chain of cholera enterotoxin.
A. Reference number: A01819; MUID: 78005537
A. Accession: A01819
A. Molecule type: protein
A. Residues: 22-38, 'H', 40-42,'N', 44-67,'T', 69-90,'N', 92-124 < KUR>
B. Lai, C.Y.
J. Biol. Chem. 252, 7249-7256, 1977
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Pred. No. 2.4e-09;
0; Mismatches 1;
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95.2%;
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A.Reference number: 514623

A.Reference number: 514623

A.Reference number: 514623

A.Reference number: 514623

A.Reference number: 514624

A.Reference number: 514646

A.Reference number: 514646

A.Reference number: 51464
A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin isol A;Reference number: A61475; MUID:89180953
A;Reference number: A61475
A;Recession: A61475
A;Molecule type: Drotein
A;Residues: 22-24, S'.26-27, E'.29-63, 'K',65-66, 'A',68-95, 'A',97-122, 'E',124 <TSU>A;Residues: 22-24, S'.26-27, E'.29-63, 'K',65-66, 'A',68-95, 'A',97-122, 'E',124 <TSU>C;Complex: the heat-labile enterotoxin molecule contains one A chain and five or six B G;Function:
A;Description: the biological activity of the toxin is produced by the A chain, which ac C;Superfamily: cholera enterotoxin beta chain
C;Superfamily: cholera enterotoxin peta chain
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-124/Product: heat-labile enterotoxin chain B #status predicted <MAT>F;30-107/Disulfide bonds: #status predicted
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95.2%; Pred. No. 1.6e-09;
11ve 0; Mismatches 1;
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Gaps

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Length 124; 1; Indels ᠬ

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Gaps

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RESULT 7
C96580
hypothetical protein F1511.6 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: O2-Mar-2001
Escential Sequence_revision 02-Mar-2001
Escential Second Sequence_revision 02-Mar-2001
C; Accession: C96580
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Anutre 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 815 820, 2000
Nature 408, 815 820, 2000
Nature 408, 815 820, 2000
Nature 5000

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A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-574 <STO>
A;Cross-references: GB:AE005172; NID:g5668763; PIDN:AAD45990.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
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Pred. No. 12;
2; Mismatches
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Pred. No. 14
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58.8%;
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Best Local Similarity
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les 12; Conser
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A, Status: preliminary
A, Molecule type: DNA
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A;Cross-references: EMBL:281482; PIDN:CAB03954.2; GSPDB:GN00028; CESP:C40H5.3
A;Experimental source: clone C40H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:U63530; NID:g1488296; PIDN:AAB65841.1; PID:g1488297
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C:Species: Caenorhabditis elegans
C:Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T19866
R:White, S.
                                                                                                                                                                                                                                       RAD23 protein homolog - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
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A;Introns: 44/2; 95/1; 178/1; 234/3; 348/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C40H5.3
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                                                                                                                                                                                                                                                                                                                                              Cyaccession: T04150
RySchultz, T.F.; Quatrano, R.S.
Rystile: Characterization and expression of a rice RAD23 gene.
RyReference number: Z08695; MUID:97369378
Rystatus: preliminary; translated from GB/EMBL/DDBJ
Ryschule type: mRNA
RyResidues: 1-392 <SCH>
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A;Molecule type: DNA
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A;Reference number: 219189
A;Accession: T19866
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42.9%; Pred. No. 3
66 GAIFQVEVPGSQHIDSQKKAI 86
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Matches 9; Conservative
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Length 374;

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Length 1742;

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Cipecies: Methanobacterium thermoautotrophicum
Cipecies: Methanobacterium thermoautotrophicum Delta H: Missis Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Glbson, R.; Jiwanl, R.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A;Recession: H69231
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE000872; GB:AE000666; NID:g2622082; PIDN:AAB85482.1; PID:g262 A;Experimental source: strain Delta H C;Genetics: A;Genetics: A;Gene: WTH985
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J. Bacteriol. 177, 5284-5288, 1995
Affitle: Sequence analysis and overexpression of the Zymomonas mobilis tgt gene encod
A;Reference number: 224129; MUID:95394847
A;Accession: T46898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C:Genetics:
A:Start codon: GTG
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A;Molecule type: DNA
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A; Cross-references: EMBL:L33777; PIDN:AAA27704.1
A; Accession: T46899
                                                                                                                                                                  DB
87;
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Pred. No. 24;
6; Mismatches
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                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                  Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                  1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.68;
36.88;
                                                                                                                                                                  41.5%;
38.1%;
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                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Rieference and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: A86457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76110
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s. Reference number: S74322; MUID:97061201
A; Reference number: S76110
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Restdues: 1-1742 cKAN>
A; Cross-references: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10088.1; PID:d101073
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                                                                                                                                                            A;Cross-references: GB:AE005173; NID:g4587538; PIDN:AAD25769.1; GSPDB:GN00141
C;Genetics:
A;Gene: F1511.6
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein AAG21605.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Aate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 R;Theologis, A.: Ecker. I P. P. 1.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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3.6;
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                                                                                                                                                                                                                                                                                                                                          Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44;
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                     Reference number: A86141; MUID:21016719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 GKTFNLEVKGSEIIQQVKNMI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 TFRVSGPGGQHRNKRDSAV 120
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 8; Conserv
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A: Residues: 1-255 <STO>
                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-91 <STO>
                                                A; Accession: C96580
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C; Species: Glycine max (soybean)
C; Species: 23-U1-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C; Accession: JG0178
R; Watanabe, A.; Nong, V.H.; Zhang, D.; Arahira, M.; Yeboah, N.A.; Udaka, K.; Fukazawa Biosci. Biotechnol. Biochem. 63, 251-256, 1999
A; Title: Molecular cloning and ethylene-inducible expression of Chibl chitinase from A; Reference number: JG0178; MUID:99208985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06221.1; GSPDB:GA;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: F83962
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20263314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: DDBJ: AB006748; NID: g4835581; PIDN: BAA77675.1; PID: g4835582 C; Superfamily: plant chitinase III C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH2502 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stress-activated protein kinase (EC 2.7.-.-) JNKb - common carp
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Pred. No. 28;
3; Mismatches 10; Indels
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     F;347-363/Domain: transmembrane #status predicted
                                                                             Score 42.5; DE
Pred. No. 29;
2; Mismatches
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166 GLTFEIEVDGGVNEETAKQCV 186
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Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                               40.1%;
62.5%;
                                                                                                                                                                                                                    Conservative
                                                                                                                                    Conservative
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                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-216 <STO>
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Matches 7; Conserv
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A; Residues: 1-299 <WAT>
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NyAlternate names: protein G2501; protein YGL148w
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C; Accession: S17246; S64162
R; Jones, D.G.L.; Reusser, U.; Braus, G.H.
Mol. Microbiol. 5, 2143-2152, 1991
MyTitle: Molecular cloning, characterization and analysis of the regulation of the ARO2 A; Reference number: S17246; MUID:92114793
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A; Residues: 1-376 <VOL>
A; Cross-references: EMBL: 272670; NID:91322731; PIDN:CAA96860.1; PID:91322732; GSPDB:GNOC
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A;Reference number: Z25018
C;Superfamily: queuine tRNA-ribosyltransferase
C;Keywords: glycosyltransferase; magnesium; metalloprotein; pentosyltransferase; tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Nap position: 3
A;Introns: 39/3; 74/1; 97/3; 138/3; 147/2; 193/3; 200/2; 273/3; 304/2; 341/3; 401/3
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N;Alternate names: protein MAA21.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun.2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49189
                                                                                                                                                               Gaps
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A; Residues: 1-376 <JONS
A; Residues: 1-376 <JONS
A; Cross-references: EMBL:X60190; NID:93386; PIDN:CAA42745.1; PID:93387
A; Volokaert, G; Voet, M; Verhasselt, P.; Defoor, E.
R; Volokaert, G; Voet, M; Verhasselt, P.; Defoor, E.
submitted to the Protein Sequence Database, May 1996
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A; Cross-references: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.110
A; Experimental source: cultivar Columbia; BAC clone MAA21
                                                                                                        Length 399;
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C;Superfamily: chorismate synthase
C;Keywords: phosphorus-oxygen lyase; transmembrane protein
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29;
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26;
                                                                                                                                                            Mismatches
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A;Cross-references: SGD:S0003116; MIPS:YGL148w
                                                                                                        Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                            134 GVTFKSHLDGSRHMLSPERSI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |::| || | | |::| 91 GKTYSMEGPGIQDCDEHNKGL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Experimental source: strain S288C
                                                                                                                                                                                                              1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                     40.6%;
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                                                                                                                                                            Conservative
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A; Accession: S64162
                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
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A; Molecule type: DNA
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Gaps

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Indels

Length 216;

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Gaps

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A, Experimental source: BAC clone B208; strain OR74A C;Genetics:
A,Gene. NCSP:B208.220
A;Map position: 6
A;Introns: 138/1
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J. Bacteriol. 171, 3673-3679, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.2%;
55.6%;
                                                                                                                                                                                                             39.68;
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A; Residues: 1-1090 <KOR>
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                               Cross-references: DDBJ:AB001744; NID:g2467307; PIDN:BAA22598.1; PID:d1023466; PID:g246 Comment: This enzyme is a mitogen-activated protein kinase, and plays a role in egg ma Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Accession: G81692
R. Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kelonay, J.; McClarty, G.; Salzberg, Nuclei Codson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kelonay, J.; McClarty, G.; Salzberg, Nuclei Caida Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:20150255
A; Accession: G81692
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-787 < TET>
A; Cross-references: GB:AE002321; GB:AE002160; NID:g7190560; PIDN:AAF39364.1; PID:g719056
A; Genetics:
A; Genetics:
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N;Alternate names: protein B208.220
S;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49574
S;Canlite, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, May 2000
A;Reference number: 22502
A;Accession: T49574
A;Accession: T49574
A;Accession: T49574
A;Beture type: DNA
A;Residues: 1-864 <SCH>
                                                   Cyperace: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999
Cyperace: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999
Cyaccession: JC5694
Ry Hashimoto, H.; Matsuo, Y.; Yokoyama, Y.; Toyohara, H.; Sakaguchi, M.
J. Blochem. 122, 381-386, 1997
A;Title: Structure and expression of carp mitogen-activated protein kinases homologous A;Reference number: JC5694
A;Accession: JC5694
A;Accession: JC5694
A;Accession: JC5694
A;Accession: JC5694
A;Accession: JC5694
A;Residues: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-427 cHAS.>
A;Cross-references: DDBJ:AB001744; NID:g2467307; PIDN:BAA22598.1; PID:d1023466; PID:g24
C;Comment: This enzyme is a mitogen-activated protein kinase, and plays a role in egg mm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inner membrane protein, probable TC0522 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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                                    Species: Cyprinus carpio (common carp)
Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999
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8
         stress-activated protein kinase b
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Pred. No. 41;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: unassigues c; C; Keywords: phosphotransferase F; 24-278/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.6%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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Matches 8; Conser
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G81692
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R;Ose1, Y.D.; Churchich, J.E. Gene 155, 185-187, 1955.
A;Title: Screening and sequence determination of a cDNA encoding the human brain 4-am A;Reference number: JC4022; MUID:95237607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: Klebsiella pneumoniae puls gene encodes an outer membrane lipoprotein requir
A:Reference number: A32880; MUID:89291709
A:Accession: A32880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. Comment: This enzyme catalyzes the conversion of 4-aminobutyrate, the inhibitory ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Klebsiella pneumon
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C;Species: Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 13-dan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S11823; A32880
R;Kornacker, M.G; Pugsley, A.P.
Mol. Microbiol, 4, 73-85, 1990
A;Ritle: Molecular characterization of pulA and its product, pullulanase, a secreted
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                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Homo sapiens (man)
C.Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 18-Jun-1999
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                                                                  Gaps
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A;Residues: 1-500 <OSE>
A;Cross-references: GB:L32961; NID:g602704; PIDN:AAA74449.1; PID:g602705
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Length 864;
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Score 42; DB;
Pred. No. 88;
3; Mismatches
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Pred. No. 59; ·
4; Mismatches
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A; Map postition: 19q13-19q13
C; Superfamily: 4-aminobutyrate transaminase
C; Keywords: aminotransferase
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A; Molecule type: mRNA
A; Residues: 1-154 < NHM
A; Comman and A; Co
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Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostellum discoideum
A;Reference number: A34080; MUID:89352609
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Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostelium discoideum
A;Reference number: A34080; MUID:89352609
                                                                               C, Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; C; Superfamily: ubiquitin/ribosomal protein degradation; ribosome; zinc f P;1-76/Product: ubiquitin #status predicted <UBI>P;1-76/Product: ubiquitin homology <UBI>P;77-128/Product: ribosomal protein CEP52 #status predicted <RIB>P;77-128/Product: ribosomal protein CEP52 pomology <CPH>P;77-128/Product: ribosomal protein CEP52 pomology <CPH>P;77-128/Product: ribosomal protein CEP52 #status predicted F;95-114/Region: zinc finger CCCC motif F;95-114/Region: nuclear location.signal
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C.Species: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
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C;Date: 30-Mar-1990 #șequence_revision 30-Mar-1990 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ubiquitin / ribosomal protein S27a – slime mold (Dictyostelium discoideum)
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C; Superfamily: polyubiquitin 3; ubiquitin homology
C; Keywords: duplication; nucleus; polyprotein; protein degradation
F; 776, Domain: ubiquitin homology <UBH2>
F; 777-152/Domain: ubiquitin homology <UBH2>
F; 153-228/Domain: ubiquitin homology <UBH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 128;
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F;102-152/Domain: ribosomal protein S27a homology <RIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubiquitin 18 - slime mold (Dictyostelium discoideum)
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20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%; Score 41; DB 1; 42.9%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Pred. No.
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Best Local Similarity
Matches 9; Conserv
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R;Ohmachi, T.; Giord
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A;Molecule type: DNA
A;Experimental source: serogroup B, strain MC58
A;Molecule to Main a; James, M.; James, M.; Molecule to M.;
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A;Residues: 1-91 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84626.1; PID:g738004
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: NMB1218; NMA1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: F81109; F81907
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Accession: F81109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein NMB1218 [imported] - Neisseria meningitidis (strain MC58 C,Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001 C;Accession: F81109; F81907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 229, 273-278, 1988
A;Title: Complete cDNA sequence of a Dictyostellum ubiquitin with a carboxy-terminal A;Reference number: S00357; MUID:88152253
A;Molecule type: mRNA
A;References: S00357
A;Molecule type: mRNA
A;Residues: 1-128 < MUE>
A;References: SMBL: X07210; NID:97381; PIDN:CAA30183.1; PID:97382
A;Experimental source: strain AX2-214
                                                                                                                                                                                                                                                                                                                       ij
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                                                                                                                                                                                                                                                                                                                            Gaps
                                     A;Cross-references: GB:M29097; NID:g342046; PIDN:AAA61976.1; PID:g643577 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                     39.2%; Score 41.5; DB 2;
llarity 38.5%; Pred. No. 1.4e+02;
Conservative 4; Mismatches 7;
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Pred. No.
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38.1%;
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|GATVQVKVENQEQLDNIYRAL
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A; Residues: 944-1090 < DEN>
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10; Conserv
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Uniquitin (clone lambda229) - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Species: Dictyostelium discoideum
C:Species: Dictyostelium discoideum
C:Species: Jo-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 06-Feb-1998
C;Accession: B27806
R;Glorda, R.; Ennis, H.L.
MOI. cell. Biol. 7, 2097-2103, 1987
A;Title: Structure of two developmentally regulated Dictyostelium discoideum ubiquitin gA; Reference number: A27806; MUID:87257921
A;Accession: B27806
A;Accession: Dippoint in 3; ubiquitin homology
C:Keywords: duplication; nucleus; polyprotein; protein degradation
F;77-152,Domain: ubiquitin homology <UBHI>F;77-152,Domain: ubiquitin homology <UBHI>F;77-152,Domain: ubiquitin homology <UBHI>F;153-228/Domain: ubiquitin homology <UBHI
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                                                                                                            Gaps
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Query Match 38.7%; Score 41; DB 2; Length 228; Best Local Similarity 42.9%; Pred. No. 31; Matches 9; Conservative 4; Mismatches 8; Indels
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Ouery Match 38.7%; Score 41; DB 2; Length 229; Best Local Similarity 42.9%; Pred. No. 31; Matches 9; Conservative 4; Mismatches 8; Indels

Search completed: July 16, 2001, 16:37:02 Job time: 211 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: July 16, 2001, 16:44:03 ; Search time 19.88 Seconds

(without alignments)
36.185 Million cell updates/sec
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(without alignmen 36.185 Million ce 36.185 Million ce Perfect score: 106 Sequence: 1 GATFQVEVPGSQHIDSQKKAI 21

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 93435

93435 seqs, 34255486 residues

Searched:

indica sactsiying chosen p

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P13811 escherichia	P32890 escherichia	P01556 vibrio chol	014896 homo sapien		P28777 saccharomyc	homo	homod	klebs	P08618 dictyosteli	-	P37535 bacillus su		P20163 caenorhabdi	Q10005 caenorhabdi			P16342 murine coro		P20220 sulfolobus	P49538 odontella s	Q9hkt0 thermoplasm	a	P51882 rattus norv	P27420 caenorhabdi	P53699 candida alb	P14882 rattus norv	P36598 schizosacch	P31870 hepatitis b	P29982 murine coro		5276 p	P13128 listeria mo
SUMMAKIES	ΩI	ELBH_ECOLI	ELBP_ECOLI	CHTB_VIBCH	IRF6_HUMAN	TGT_ZYMMO	AROC_YEAST	ST14_HUMAN	GABT_HUMAN	PULA_KLEPN	UBIQ_DICDI	YP68_CAEEL	YAAN_BACSU	PMS2_HUMAN	HS74_CAEEL	YRY1_CAEEL	YDH2_SCHPO	RPC_BPPHC	RRPB_CVMA5	INR1_SHEEP	Y13K_SSV1	YC43_ODOSI	SR54_THEAC	IL7R_MOUSE	CD5_RAT	HS7C_CAEEL	CC4_CANAL	PCCA_RAT	THI1_SCHPO	DPOL_HPBVM	RRPB_CVMJH	CHIA_CICAR	- 1	TACY_LISMO
	Length DB	124 1	124 1	124 1	467 1	385 1	376 1	855 1	500 1	1090 1	76 1	313 1	386 1	862 1	288 1	355 1	655 1	683 1	2733 1	560 1	112 1	263 1	456 1	459 1	491 1	661 1	684 1	704 1	775 1	842 1	2731 1	293 1	344 1	529 1
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	Score	106	101	100	44	4	42.5	42	41.5	41.5	41	41	41	40.5	40	40	40	40	-	39.5	39	39	39	39	39	39	39	39	39	39	39	38.5	38.5	38.5
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P55305 emericella P13117 neurospora 09953 aeropyrum p 049436 mycoplasma P75118 mycoplasma P40914 kluyveromyc P43563 aeccharomyc P31212 solanum tub P29405 rhizopus ni P89216 thogotto vir	087905 bacillus th
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                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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"Crystal structure of the B subunit of escherichia coli heat-labile
                       enterotoxin carrying peptides with anti-herpes simplex virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85156481; PubMed-3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit
cistrons from Escherichia coli of human and porcine origin.";
Infect. Immun. 48:73-77(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dallas W.S., Falkow S.; Amino acid sequence homology between cholera toxin and Escherichia
                                                                      -1- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-1- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P32890; P13768; P01557; P32890; P13768; P01557; P32800; P1396 (Rel. 01, Created) P10V-1996 (Rel. 32, Last sequence update) P15-JUL-1998 (Rel. 36, Last annotation update) PORCINE (LTP-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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H -> Y (IN ISOLATE H10407).
H -> R (IN ISOLATE H10407).
E9F7F7C7B9D3BC47 CRC64;
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                                                              Chem. 274:8764-8769(1999)
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MEDLINE=81074965; PubMed=7003397;
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                                                                                                                                                                                                                                                                                                                                 EMBL, M17874; AAA98064.1; -. EMBL, 101646; AAB02982.1; -. EMBL, 560731; AAC60441.1; -. EMBL; X83966; CAA58800.1; -.
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Nature 288:499-501(1980)
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InterPro; IPR001835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Crystal structure of a cholera toxin-related heat-labile enterotoxin
                               MEDLINE-87137303; PubMed-3546273;
Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic
Esoherichia coli and Vibrio cholerae Ol.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-91238966; PubMed-2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M., Witholt B., Hol W.G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.;
Kefined structure of Escherichia coli heat-labile enterotoxin, a
close relative of cholera toxin.";
J. Mol. Biol. 230:890-918 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.; Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.; Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae."; Mol. Microbiol. 15:1165-1167(1995).

-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                   SEQUENCE OF 1-22 FROM N.A.
MEDIINE-87280041; PubMed-3301830;
Ibrahimi I., Gentz R.;
"A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmic
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MEDLINE-93240541; PubMed-8478941;
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                                                                                                                                                                                               J. Bacteriol. 169:1352-1357(1987).
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EMBL; M15363; AAA24792.1; -.
EMBL; M17101; AAA23973.1; -.
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Nature 351:371-377(1991).
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STRAIN-ISOLATE PCG86;
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1LTB; 31-JAN-94
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1LTS; 31-JAN-94
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PDB; 1LT6; 03-DEC-97
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PIR; B26946; QLECEB.
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STRAIN=EL TOR 2125;
MEDLINE=84068199; PubMed=6646234;
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
Honda T.;
                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                 MEDLINE-84061784; PubMed-6315707;
Lockman H., Kaper J.B.;
"Nucleotide sequence analysis of the A2 and B subunits of Vibrio
                                                                                                                                                                                                                                                                                                                                                                                "Cholera toxin genes: nucleotide sequence, deletion analysis and vaccine development.";
Nature 306:551-557(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=4260B / SEROTYPE 0139;
MEDILINE-94237453; PubMed-8181723;
Lebens M., Holmgren J.
"Structure and arrangement of the cholera toxin genes in Vibrio
                                                                                                                                          ;
                                                                                                                          Length 124;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=EL TOR 2125;
Dams E., de Wolf M.,
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                     14133 MW; 6DB7DE58395EA70D CRC64;
                                                                                                                  CHTB_VIBCH STANDARD; PRT; 124 AA. P01556; Q9JQ02; 21-JUL-1986 (Rel. 01, Created) 13-AGC-1987 (Rel. 05, Last sequence update) 10-CT-2000 (Rel. 40, Last annotation update) CHOLERA ENTEROTOXIN, BETA CHAIN PRECURSOR. CTXB OR TOXB OR VC1456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMS Microbiol. Lett. 117:197-202(1994),
                                                                                                                                                                                                                                                                                                                      cholerae enterotoxin.";
J. Biol. Chem. 258:13722-13726(1983)
                                                                                                                                                               66 GETFQVEVPGSQHIDSQKKAI 86
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STRAIN=1854 / Ol39-BENGAL;
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SEQUENCE FROM N.A.
SEROTYPE 01;
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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-!- SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN
(FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAIN
DISULFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO
6 BETA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Determination of the primary structure of cholera toxin B subunit."; J. Biol. Chem. 252:7249-7256(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure of cholera toxin B-pentamer bound to receptor GM1 pentasaccharide.";
Protein Sci. 3:166-175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE-97376625; PubMed-9232653;
Merritt E.A., Sarfaty S., Jobling M.G., Chang T., Holmes R.K.,
Hirst T.R., Hol W.G.J.;
"Structural studies of receptor binding by cholera toxin mutants.";
Protein Sci. 6:1516-1528(1997).
-: FUNCTION: THE BETA CHAIN AGGREGATE (B SUBUNIT) IS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95387394; PubMed-7658472;
Zhang R.G., Westbrook M.L., Westbrook E.M., Scott D.L., Otwinowski
Maulik P.R., Reed R.A., Shipley G.G.;
"The 2.4 A crystal structure of cholera toxin B subunit pentamer:
choleragenoid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-94272319; PubMed-8003954;
Merritt E.A., Sarfaty S., van den Akker F., L'Hoir C., Martial J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 22-124.
MEDLINE-78005337; PubMed=903363;
Kurosky A., Markel D.E., Peterson J.W.;
"Covalent structure of the beta chain of cholera enterotoxin.";
J. Biol. Chem. 252:7257-7264(1977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 22-124.
MEDLINE-78005536; Pubmed-903362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Mol. Biol. 251:550-562(1995).
[11]
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EMBL; X76391; CAA53976.1; --
EMBL; AE004224; AAF94613.1;
PIR; A01819; XVVCB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
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MEDLINE-9625633; Pubmed-863483;
ROmier C., Reuter K., Stoner R.;
"Crystal structure of tRNA-guanine transglycosylase: RNA modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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STRAIN-ATCC 31821 / LM4 / CP4;
MEDLINE-92406015; Pubmed-1526462;
Shark K.B., Conway T.;
"Cloning and molecular characterization of the DNA ligase gene (lig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
Graedler U., Gerber H.D., Goodencough-Lashua D.M., Garcia G.A.G.,
Figner R., Reuter K., Stubbs M.T., Klebs G.;
"A new target for shigellosis: rational design and crystallographic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95394847; PubMed-7665516;
Reuter K.H., Ficner R.;
"Sequence analysis and overexpression of the Zymomonas mobilis tyt gene encoding tRNA-guanine transglycosylase: purification and biochemical characterization of the enzyme.";
J. Bacteriol. 177:5284-5288(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGT_ZYMMO STANDARD; PRT; 385 AA.

928720; 060247;
01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0-MAY-2000 (Rel. 39, Last annotation update)
UDEUINE TRNA-REDSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRNA-RELEASE) (GUANINE INSERTION ENZYME).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Length 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., SEQUENCE OF 1-6, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; DNA-binding; Nuclear protein.
DNA-BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
SEOUENCE 467 AA; 53129 MW; 7E28F5E0F5BA4053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.5%; Score 44; DB
41.2%; Pred. No. 11;
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-! - SIMILARITY: BELONGS TO THE IRF FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Zymomonas mobilis.";
FEMS Microbiol. Lett. 75:19-26(1992).
                                                                                                                                                                                                                                                                                              EMBL; AF027292; AAB84111.1; -.
EMBL; AL022398; CAA18345.1; -.
HSSP; P23906; ILRG.
INTERPLO; IPR001346; -.
Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTERNEGFCT.
PROSITE; PS00601; IRF; 1.
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EMBO J. 15:2850-2857(1996).
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Matches 7; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHOLERA ENTEROTOXIN, BETA CHAIN.
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95.2%; Pred. No. 1.9e-09;
ive 0; Mismatches 1; Indels
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grossman A., Mittrucker H.W., Antonio L., Ozato K., Mak Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERFERON REGULATORY FACTOR 6 (IRF-6).
                                                                                                                                                                                                                                                                                                                                                                                                                         Membrane; Enterotoxin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA
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                                                                                                                                                                                                                                                                                              TIGR: VC1456; --
InterPro: IRFO01835; --
Pfam: PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
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                  PIR; S14624; S14624.
PDB; 3CHB; 03-DEC-97.
PDB; 1CHP; 08-MAR-96.
PDB; 1CHQ; 08-MAR-96.
PDB; 1FGB; 23-DEC-96.
PDB; 1FGB; 23-DEC-96.
PDB; 1XPB; 01-APP-97.
PDB; 1XTC; 01-APP-97.
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15-JUL-1998 (Rel. 36,
15-JUL-1999 (Rel. 38,
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Query Match Best Local

Matches

IRF6_HUMAN 014896;

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MEDLINE-92114793; PubMed-1837329;
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Q9Y5Y6;
                                                                                             cerevisiae
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ST14_HUMAN
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      ID DATE OF THE SERVICE OF THE SERVIC
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                             -!- SUBUNIT: MONOMER.
-!- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
-!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY DUE
studies of inhibitors of trnA-guanine transglycosylase.";
Submitted (MAR-2000) to the PDB data bank.
-!- FUNCTION: EXCHANGES THE GUANINE RESIDUE WITH 7-AMINOMETHYL-7-
DEAZAGONAINE IN TRNAS WITH GU(N) ANTICODONS (TRNA-ASP, -ASN, -HIS
AND -TYR). AFTER THIS EXCHANGE, A CYCLOPENTENDIOL MOIETY IS
ATTACHED TO THE 7-AMINOMETHYL GROUP OF 7-DEAZAGONAINE, RESULFING
IN THE HYPERMODIFIED NUCLEOSIDE GUEDOSINE (Q) (7-((14.5-CIS-
DIHYDROXY-2-CYCLOPENTEN-1-YI)AMINO)METHYL)-7-DEAZAGUANOSINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                           CATALYTIC ACTIVITY: TRNA GUANINE + QUEUINE = TRNA QUEUINE +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Queuosine biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F3D6FA270A0B23F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tRNA processing; Zinc; Magnesium; 3D-structure.
INIT_MET 0 0
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EMBL; L33777; AAA27705.1; ALT_INIT.
EMBL; Z11910; -; NOT_ANNOTATED_CDS.
PDB; 1PUD; 07-JUL-97.
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PDB; IWKE; 07-001-97.
PDB; IWKF; 07-001-97.
PDB; IEWU; 19-APR-00.
InterPro; IPR002616; -
Pfam; PF01702; TGT; 1.
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280
317
319
322
348
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Best Local Similarity
Matches 8; Conserv
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P28777;
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ACT_SITE
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=97197983; PubMed=9046099;

MEDLINE=97197983; PubMed=9046099;

MEDLINE=97197983; PubMed=9046099;

MEDLINE=97197983; PubMed=9046099;

MEDLINE=97197983; PubMed=9046099;

NOTICE TIPLY

TIPLY Genes and stance open reading frames.";

TIPLY MREY genes and stance open reading frames.";

Yeast 13:177-182(1997).

COPALYTIC ACTIVITY: 5-0-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE =

CHORISMATE + ORTHOPHOSPHATE.

COPACTOR: REDUCED FLAVIN.

COPACTOR: REDUCED FLAVIN.

THE BIOSYNTHESIS OF AROMATIC ANINO ACIDS (THE SHIKIMATE PATHWAY).

COPACTOR: BY AMINO ACID STRAYMINO.

COPACTOR: BY AMINO ACID STRAYMINO.

COPACTOR: BY AMINO ACID STRAYMINO.
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01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
SUPRESSOR OF TUMORIGENICITY 14 (EC 3.4.21.-) (MATRIPTASE) (MEMBRANE-
TYPE SERINE PROTEASE 1) (MT-SP1).
Jones D.G.L., Reusser U., Braus G.H.; Molecular cloning, characterization and analysis of the regulation of the AROZ gene, encoding chorismate synthase, of Saccharomyces perevisiae ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-99303581; PubMed=10373424;
Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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Pfam; PF01264; Chorismate_synt; 1.
PROSITE: PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.
Lyase; Aromatio acid blosynthesis.
SEQUENCE 376 AA; 40838 MW; AF3AF6560SB91E8E CRC64;
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                                                                                                                                              Mol. Microbiol. 5:2143-2152(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60190; CAA42745.1; -. EMBL; X99960; CAA68214.1; -. EMBL; Z72670; CAA96860.1; -. PIR; S17246; S17246.
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Matches 10; Conservative
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                                                                                                   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
"Molecular cloning of cDNA for matriptase, a matrix-degrading serine
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                                         Takeuchi T., Shuman M.A., Craik C.S.;
"Reverse blochemistry: Use of macromolecular protease inhibitors the dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";
Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
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CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
N-LINKED GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
CATALYTIC.
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        protease with trypsin-like activity.";
J. Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO026; LDLEECEPTOR.
PRINTS; PRO0722; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS01134; TRYPSIN_ER; 1.
PROSITE; PS01130; CUB; 2.
PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS0068; LDLRA_1; 2.
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InterPro; IPR002172; -.
Pfam; PF00057; Idl_recept_a; 4.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                               EMBL; AF118224; AAD42765.2; -. EMBL; AF133086; AAF00109.1; -.
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                                  SEQUENCE FROM N.A.
                                                                                             CHARACTERIZATION.
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                                                                                                                                                                                   Gaps
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Nyhan W.L., Gibson K.M.;
"4-aminobutyrate aminotransferase (GABA-transaminase) deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT DEFICIENCY WHOSE PHENOTYPE INCLUDES PSYCHOMOTOR RETARDATION, HYPOTONIA, HYPERREFLEXIA, LETHARGY, REFRACTORY SEIZURES, AND EEG
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-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: MONOMER (PROBABLE).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- TISSUE SPECIFICITY: LIVER > PANCREAS > BRAIN > KIDNEY > HEART >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Biase D., Barra D., Simmaco M., John R.A., Bossa F.; "Primary structure and tissue distribution of human 4-aminobutyrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
N-LINKED (GLCNAC. .) (POTENTIAL) 26143132C01F99C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-ANINOBUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.19) (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA AMINOTRANSFERASE) (GABA-AT).
                                                                                                                      Length 855
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                                                                                                                                                                                Mismatches
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                                                                                                                         Score 42;
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Eur. J. Biochem. 227:476-480(1995)
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MEDLINE=95237607; PubMed=7721088;
                                 94769 MW;
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50.0%;
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                                                                                                                                                                                   6; Conservative
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367 TWNIEVPNNQHV 378
                                                                                                                                                                                                                                          3 TFQVEVPGSQHI 14
                                 855 AA;
                                                                                                                      Query Match
Best Local Similarity
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      CARBOHYD
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CONFLICT
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MEDLINE-86033621; PubMed-3902792;
Chapon C., Raibaud O.;
"Structure of two divergent promoters located in front of the gene encoding pullulanase in Rlebsiella pneumoniae and positively regulated by the malT product.";
J. Bacteriol. 164:639-645(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1988 (Rel. 07, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Est annotation update)
PULLULANASE PRECURSOR (EC 3.2.1.41) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE) (PULLULAN 6-GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kornacker M.G., Pugsley A.P.; "Molecular characterization of pulA and its product, pullulanase, secreted enzyme of Klabsiella pneumoniae UNF5023."; Mol. Microbiol. 4:73-85(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                    4-AMINOBUTYRATE AMINOTRANSFERASE.
PYRIDOXAL PHOSPHATE.
R -> K (IN GABA-AT DEFICIENCY; 25%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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D'Enfert C., Pugsley A.P.;
"Klebsiella pneumoniae pulS gene encodes an outer membrane lipoprotein required for pullulanase secretion.";
J. Bacteriol. 171:3673-3679(1989).
                                           InterPro: IPR000954; - ... 3; 1. Pfam; PF00202; aminotran_3; 1. PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1. Transferase; Aminotransferase; Pyridoxal phosphate; Mucotransmitter degradation; Mitochondrion; Transit peptide; Disease mutation.
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-> H (IN REF. 2).
41199085693F80AD CRC64;
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EMBL; L32961; AAA74449.1; -. MIM; 137150; -.
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17 TYRLLVPGSRHI-SQAAA 33
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Best Local Similarity 55.6
Matches 10; Conservative
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P07206;
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                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                      -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
(1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO FORM MALTOTRIOSE.
                                                                       SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (PROBABLE).
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C IN REF. 2).
V -> F (IN REF. 2).
V -> I (IN REF. 2).
G -> S (IN REF. 2).
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PROBITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Hydrolase; Glycosidase; Membrane; Lipoprotein; Signal.
SIGNAL 1
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostellum.
NCBL_TaxID=44689;
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Last annotation update)
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Matches 10; Conservative
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                                                   SUBUNIT: HOMOTRIMER.
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PIR; A32880; A32880.
PIR; S11823; S11823.
InterPro; IPR000461; -.
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                                                                                                                                                                                                            Westphal M., Mueller-Taubenberg A., Noegel A., Gerisch G.;
"Transcript regulation and carboxyterminal extension of ubiquitin in
Dictyostellum discoideum";
FEBS Lett. 209:92-96(1986).
-I- FUNCTION: INVOLUED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF
CELLULAR PROPEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE
REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                       MEDLINE-87257921; PubMed-3037345;
Giorda R., Ennis H.L.;
"Structure of two developmentally regulated Dictyostelium discoideum
ubiquitin genes.";
                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES
CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
           MEDLINE-89352609; PubMed-2548604;
Ohmachi T., Giorda R., Shaw D.R., Ennis H.L.;
"Molecular organization of developmentally regulated Dictyostelium
discoldeum ubiquitin CDMAS.";
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COUJUGATION TO ACCEPTOR PROTEINS.
K -> N (IN SOME CLONES REPEATS).
6427383968EA884 CRC64;
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AAA33262.1; ALT_TERM.
AAA33264.1; ALT_TERM.
AAA33266.1; ALT_TERM.
AAA33266.1; ALT_TERM.
AAA33266.1; ALT_TERM.
AAA33268.1; ALT_TERM.
AAA33268.1; ALT_TERM.
AAA33268.1; ALT_TERM.
                                                                                                                                               ubiquitin genes.";
Mol. Cell. Biol. 7:2097-2103(1987).
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EMBL; M19466; AAA32261.1; ALT_TERM
EMBL; M19491; AAA3260.1; ALT_TERM
EMBL; M29748; AAA32200.1; ALT_TERM
EMBL; M23748; AAA33262.1; ALT_TERM
EMBL; M23749; AAA33263.1; ALT_TERM
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PROSITE; PS50053; UBIQUITIN_2; 1.
                                                               Biochemistry 28:5226-5231(1989)
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PIR; A27806; A27806.
PIR; B34080; A34080.
PIR; B34080; A34080.
PIR; C34080; B34080.
PIR; C34080; D34080.
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                                                                                           SEQUENCE FROM N.A.
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M23752;
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Score 41; DB 1; Length 76;

38.7%;

Query Match

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NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogasawara N., Makai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin."; Bacillus Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
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01-OCT-1994 (Rel. 30, Last sequence update)
01-EEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 43.8 KDA PROTEIN IN XPAC-ABRB INTERGENIC REGION.
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  Indels
                                                                                                                                                                                                                      01-Nov-1997 (Rel. 35, Created)
01-Nov-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 37.0 KDA PROTEIN B0495.8 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36977 MW; 000D2327621BFED0 CRC64;
æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1;
Pred. No. 23;
                                                                                                                                                                                  313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,
                                                               | | :|| || :|: | |
GKTITLEVEGSDNIENVKAKI 30
                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U21317; AAA62527.1; -. WormPep; B0495.8; CE01766. Hypothetical protein. SEQUENCE 313 AA; 36977 MW.
                                          GATFQVEVPGSQHIDSQKKAI
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 EVPGSQHIDSQKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: ||||:|:::|
11 QLMGSQHVDNKEK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirsten J.;
                                                                                                                                                                                  YP68_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAAN_BACSU
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9

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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
HS74_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBUNIT: HETERODIMER OF PMS2 AND MLHI.
-i- DISEASE: ASSOCIATED WITH FAMILIAL HEREDITARY NONPOLYPOSIS COLON
CANCER (HNPCC) (LYNCH SYNDROME). HNPCC IS ONE OF THE MOST COMMON
GENETIC DISEASES IN THE WESTERN WORLD, AND ACCOUNTS FOR 15% OF ALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bronner C.E., Baker S.M., Morrison P.T., Warren G., Smith L.G., Lescoe M.K., Kane M., Earibino C., Lipford J., Lindblom A., Tannergaard P., Bollag R.J., Godwin A.R., Ward D.C., Nordenskjoeld W., Fishel R., Kolodner R.D., Liskay R.M.; Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2).
PMS2 OR PMS12.
Endo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Endometrial tumor;
MEDLINE-94352394; PubMed-8072530;
MICOLAIdes N.C., Papadopoulos N., Liu B., Wei Y.-F., Carter K.C.,
Ruben S.M., Rosen C.A., Haseltine W.H., Fleischmann R.D.,
Fraser C.M., Adams M.D., Venter J.C., Dunlop M.G., Hamilton S.R.,
Petersen G.M., de la Chapelle A., Vogelstein B., Kinzler K.W.;
"Mutations of two PMS homologues in hereditary nonpolyposis colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1; Length 386; Pred. No. 28;
SEQUENCE OF 1-191 FROM N.A.
Bookstein C., Edwards C.W., Hulett F.M.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                            E -> M (IN REF. 2).
D921F3A0F6845EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
CONFLICT 191 191 E
SEQUENCE 386 AA; 43830 MW;
                                                                                                                                                                                                                                                                                       EMBL; D26185; BAA05262.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.78;
31.28;
                                                                                                                                                                                                                                                                                                                  EMBL; M96156; AAA22892.1;
EMBL; Z99104; CAB11802.1;
SubtiList; BG10090; yaan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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22 IEIPGSEAVKAEKEQV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 371:75-80(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMS2_HUMAN
P54278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMS2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPROT IPRO010286. -
Interpror IPR0010286. -
Fam. PF00121 HSP70: 1.
PROSITE: PS00014; ER_TARGET: 1.
PROSITE: PS000329; HSP70_2: PARTIAL.
PROSITE: PS01036; HSP70_2: PARTIAL.
PROSITE: PS01036; HSP70_2: PARTIAL.
ATP-binding; Heat shock; Endoplasmic reticulum; Multigene family.
STE 285 288 PA; 31267 MW; 967F5A4A12FA67BF CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Identification of a heat-shock pseudogene from Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 862;
                                                                                                                                                                                                                                                                                                                                                                            MIM; buves,
http://www.news.com/mis.repair; 1.
http
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 P -> S (IN REF. 2).
95797 MW; B60A605222CBBCAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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15-JUL-1998 (Rel. 36, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN D (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE-89306577; PubMed-2744444;
Heschl M.F.P., Baillie D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                           EMBL; U13696; AAA63923.1; -. EMBL; U14658; AAA50390.1; -. SWISS-2DPAGE; P54278; HUMAN. MIM; 600259; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M28528; AAA28076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome 32:190-195(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO MAMMALIAN GRP78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| |:|||:||
528 GSQEHVDSQEKA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GSQ-HIDSQKKA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        862 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSP-4 OR HSP70D
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us-09-786-648-4.rsp

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Bacteriophage phi-C31.
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                                                                              Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=4896;
    SPAC6G9.02C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPC_BPPHC
P08979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPC_BPPHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 39.9 KDA PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.
T15H9.1.
                                                          ;
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                      Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.7%; Score 40; DB 1; Length 355;
47.4%; Pred. No. 38;
tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN T15H9.1.
                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases -! - SIMILARITY: CONTAINS 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 75.4 KDA PROTEIN C6G9.02C IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95FA4D8E551D9CC2 CRC64;
                    DB 1;
                                                                                                                                                                                                                                    355 AA
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PF00226; DnaJ; 1.
Pfam: PF01556; DnaJ_C; 1.
PROSITE: PS00636; DNAJ_1; 1.
PROSITE: PS50076; DNAJ_2; 1.
Hypothetical protein; Chaperone;
                                                        9
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                  37.78;
35.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 247356; CAA87414.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 TFDVEFPKTELSDEQKAQI 338
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                                                                                                                  CE01664.
                                                                                              3 TFQVEVPGSQHIDSQKK 19
                                                          Conservative
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                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MormPep; T1549.1; CE016
InterPro; IPR001623; -.
InterPro; IPR002939; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
Query Match
Best Local Similarity
'-hag 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P08622; 1XBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116
355 AA;
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gardner A.;
                                                                                                                                                                                                                                  YRY1_CAEEL
Q10005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDH2_SCHPO
Q92347;
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  temperate phage
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"The repressor gene (c) of the Streptomyces temperate phage phi c31:
mucleotide sequence, analysis and functional cloning.";
Mol. Gen. Genet. 213:269-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Lambda phage group.
NCBL_TaxID=10719;
                                                                                                                                                                                                                                                           Murphy L., Harris D., Barrell B.G., Rajandream M.A., Connor R.E.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
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HartLey N.M., Mirphy G.O., Bruton C.J., Chater K.F.;
"Sequence of the essential early region of phi C31, a te
of Streptomyces spp. with unusual features in its lytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001313; -.
Pfan, PF00806; PUF; 5.
Hypothetical protein.
SEQUENCE 655 AA; 75440 MW; 45E6C4491692DA42 CRC64;
                           Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
REPRESSOR PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
73;
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Schizosaccharomyces pombe (Fission yeast).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z81317; CAB03604.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.78;
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DISULFID
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MEDLINE-9024573; PubMed-2159623;

MEDLINE-9024573; PubMed-2159623;

MEDLINE-9024573; PubMed-2159623;

Mediss S.R., Span W.J.M.;

The primary structure and expression of the second open reading frame of the polymerase gene of the coronavirus MHV-A59; a highly conserved polymerase gene of the coronavirus MHV-A59; a highly frameshifting mechanism."; and efficient ribosomal frameshifting mechanism."; CONSERVED STRUCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS A MULTIFUCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY FOR THE TRANSCRIPTION PROCEDING STRANDED RNA, LEADER RNA, SUBGENOMIC MANAS AND PROCEDING YIRION RNA.

C. CATALITIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine coronavirus MHV (strain A59).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A polymerase; Helicase; ATP-binding.
POLYMERASE.
CYS/HIS-RICH.
HELICASE.
                                                                                                                                                                                         .;
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                                                                                                                                                     37.7%; Score 40; DB 1; Length 683; 50.0%; Pred. No. 76;
                                                                                                                                                                                         Indels
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IN; F3ACC8EF20D20C41 CRC64;
                                                               PIR; S01433; S01433.
Transcription regulation; Repressor; DNA-binding.
SEQUENCE 683 AA; 74077 MW; B02379D204F37D1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B).
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                                                                                                                                                                                                                                                                                                                                                 PRT; 2733 AA.
                                                                                                                                                                                        2; Mismatches
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X51939; CAA36202.1; ALT_SEQ. PIR; S08652; S08652. PIR; S15760; S15760.
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                              EMBL; X12865; CAA31345.1; -. EMBL; X76288; CAA53911.1; -.
                                                                                                                                   Ouery Match
Best Local Similarity 50...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                              | || |: |: ||
86 GRTFDTELTGADHI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227
                                                                                                                                                                                                                          1 GATFQVEVPGSQHI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11142;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               P16342;
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SWADACC
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Gaps

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Score 40; DB 1; Length 2733; Pred. No. 3.4e+02; 2; Mismatches 6; Indels

2; Mismatches

8; Conservative

Query Match Best Local Similarity Matches 8; Conserv

37.7%; 50.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pregnancy.";
Endocrinology 138:4757-4767(1997).
-i- FUNCTION: RECEPTOR FOR INTERPERONS ALPHA AND BETA. BINDING TO TYPE
-I FUNCTION: RECEPTOR FOR INTERPERONS ALPHA AND BETA.
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT CONCEPTUS AT DAY 15 OF PREGNANCY.
-- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                 INRI_SHEEP STANDARD; PRT; 560 AA. 028589; 095206; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) INTERPERON ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC) (INTERPERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                                                         Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-98006426; PubMed-9348203; Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.; Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                            Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F., "Structure of an ovine interferon receptor and its expression in endometrium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERFERON-ALPHA/BETA RECEPTOR ALPHA
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Endocrinol. 17:207-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Endometrium;
MEDLINE=97135690; PubMed=8981227;
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                              1199 TFONNVPNYOHIGMKR 1214
3 TFQVEVPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                               Bovidae; Caprinae; Ovis.
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458
560
84
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47
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55
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Pfam; PF00041; fn3; 1
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9940;
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438
459
76
199
47
85
                                                                                                                                                                                                                                          IFNAR1 OR IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    endometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
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TRANSMEM
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HYPOTHETICAL 30.1 KDA PROTEIN YCF43 (ORF263).
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Best Local Similarity
'-hag 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
241
263 AA;
                                                                                                                                                                                                                                                                                  Odontella sinensis.
                                                      Odontella sinensis
                                                                                                                                                                                                       SEQUENCE FROM N.A. Kowallik K.V., Sto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SR54_THEAC
Q9HKT0;
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TRANSMEM
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MEDLINE-92024080; Pubmed-1926776;
Pallm P., Schleper C., Grampp B., Yeats S., McWilliam P., Reiter W.-D.
21111g W.;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Viruses; dsDNA viruses, no RNA stage; Fusellovirus.
                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
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-> D (IN REF. 2).
E7198A1905D4805C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete nucleotide sequence of the virus SSV1 of the archaebacterium Sulfolobus shibatae.";
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112 AA; 13204 MW; 23F9C02D979AF383 CRC64;
                                                                                                     (GLCNAC. . .)
N-LINKED (GLCNAC...
N-LINK
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01-FRB-1991 (Rel. 17, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
HYPOTHETICAL 13.2 KDA PROTEIN (ORF F-112).
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 Score 39.5; D. Pred. No. 74; 4; Mismatches
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Best Local Similarity 37.5%;
Matches 9; Conservative
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                                                                                                                            313
359
377
434
352
522
560 AA;
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Hypothetical protei
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hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10476;
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P49538;
01-FEB-1996 (
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01-OCT-2000
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X13K_SSV1
ID X13K_SSV1
AC P20220;
                                                                                                  CARBOHYD
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YC43_ODOSI
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                                                                                                                                                                   Freier U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acidophilum.";
Nature 407:508-513(2000).
-1- UNCTION: BINDS TO THE SIGNAL SEQUENCE OF PRESECRETORY PROTEIN
WHEN THEY EMERGE FROM THE RIBOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                        Plant MOL. Biol. Rep. 13:336-342(1995).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE TATC FAMILY.
Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBL_TaxID=2839;
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                                                                                                                                                                Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Frei
"The chloroplast genome of a chlorophyll a+c-containing alga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 263;
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40;
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01-0cT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
SIGNAL RECOGNITION 54 KDA PROTEIN (SRP54).
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MEDLINE-20479972; PubMed-11029001;
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NCBI_TaxID=10116;
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TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
-!- SUBUNIT: ARCHAEAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA MOLECULE OF 300 NUCLEOTIDES AND TWO PROTEIN SUBUNITS: SRP54 AND SRP19 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- DOMAIN: HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE 7S RNA. IN PRESENCE OF SRP19 AND ALSO BINDS THE SIGNAL SEQUENCE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: RECEPTOR FOR INTERLEUKIN-7.
-i- SUBGNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
-i- SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: SPLEEN; TYYMUS; AND FETAL LIVER.
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i- SIMILARITY: CONTAINS I FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodwin R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A., Gimpel S., Cosman D., Dower S.K., March C.J., Namen A.E., Park L.S. "Cloning of the human and murine interleukin-7 receptors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     demonstration of a soluble form and homology to a new recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal recognition particle; GTP-binding; RNA-binding.
DOMAIN 1 289 G-DOMAIN (BY SIMILARITY).
DOMAIN 290 456 M-DOMAIN (BY SIMILARITY).
NP_BIND 104 111 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6560FA972DA3EA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB Pred. No. 72; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51080 MW;
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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188
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Cell 60:941-951(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 IPGSQKIDDSK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 VPGSQHIDSQK 18
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P16872;
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SEQUENCE
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30-MAY-2000 (Rel. 39, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LYMPHOCYTE GLYCOPROTEIN LY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                               SER/THR-RICH.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

PHOSPHORYLATION (BY PKC) (POTENTIAL).

CC06A5CE95543849 CRC64;
                                                                                                                                                                                                                                             INTERLEUKIN-7 RECEPTOR ALPHA CHAIN
                                                                                                                                                                                            Receptor; Transmembrane; Glycoprotein; Phosphorylation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Length 459;
Pred. No. 72;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murakami T.;
Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING T-CELL PROLIFERATION. CD5 INTERACTS WITH CD72/LYB-2.
-!- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS 2 SRCR DOMAINS.
                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal, Transmembrane, Glycoprotein, T-cell.
SIGNAL
1 23 BY SIMILARITY.
CHAIN 24 491 T-CELL SURFACE G
DOMAIN 25 368 EXTRACELLULAR (F
TRANSMEM 369 398 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA.
                                                                                                                                                                        PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR01190; -.
Pfam; PF00530; SRCR; 3.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1) (LYT-1) (LYMPHOCYTE ANTIGEN CD5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D10728; BAA01571.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.8%;
EMBL; M29697; AAA39304.1;
PIR; D34791; D34791.
MGD; MGI:96562; Il7r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
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                                                                    InterPro; IPR000950; -. InterPro; IPR001777; -. InterPro; IPR002465; -. Pfam; PF00041; fn3; 1.
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459
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459 AA;
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Best Local Similarity
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                                                                                                                                                                 ö
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULÀR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY. STRONG, TO MAMMALIAN GRP78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
MEDLINE-89356251; PubMed-2766926;
Heschl M.F.P., Baillie D.L.;
"Characterization of the hsp70 multigene family of Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01035; HSP70_3; 1.
ATP-binding; Heat shock; Endoplasmic reticulum; Multigene family;
                                       POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
88DD76F8E6891CDE CRC64;
                                                                                                                                                                 ;
0
                                                                                                                                      1; Length 491;
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HEAT SHOCK 70 KDA PROTEIN C.
HEAVENT SECRETION FROM ER.
7F5CD624F48293BA CRC64;
                                                                                                                                                                 3; Indels
 CYTOPLASMIC (POTENTIAL)
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HSP-3 OR HSP70C.
                                                                                                                                                                                                                                                                                      661 AA
                                                                                                                                     Score 39; DB Pred. No. 78; 4; Mismatches
                                                                                                                                      DB 78;
              SRCR 1.
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PIR; A32475; A32475.
HSSP; P19120; ING;.
InterPro; IPR001086; -.
InterPro; IPR001023; -.
Pfam; PF00012; HSP70; 1.
                                                                                                                                      36.8%;
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Best Local Similarity 35.3
Matches 6; Conservative
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436 QVENPAASHVDNE 448
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Best Local Similarity
Matches 6; Conservat
                                                                   176
239
491 AA;
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DNA 8:233-243(1989)
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658
661 AA;
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P27420;
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CARBOHYD
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Gaps

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505 TFEIDVNGILHVTAEDK 521
3 TFQVEVPGSQHIDSQKK 19
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022511 vitis vinif Q43098 psophocarpu Q97690 leishmania C27066 methanobact Q9f517 zymomonas m Q91y67 arabidópsis Q9kx22 baciltús ha Q9sxm5 glyčine max Q9syg9 gfycine max Q9hb36 Acmo sapien

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                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                       1 GATFQVEVPGSQHIDSQKKAI 21
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           US-09-786-648-4
106
                                                                                                                                                                                                                                                                     Perfect score:
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Run on:

022511 043098 098792 027066 027066 027066 098927 098922 098822 098823 099823 099823 099833 099730 004636 004636

ALIGNMENTS

40.5 40.5 40.5

425026

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_16:*

Database

425026 seqs, 132305027 residues

Searched:

Q9bb36 Anno sapien O42099 cyprine aca Q9pke3 chlamydia m Q9bca3 homo sapien Q9bs3 homo sapien Q9bs3 homo sapien Q9bs2 neurospora Q9jri4 neisseria m Q9v9u6 drosophila Q9sq79 pinus taeda O91529 hepatitis b Q9qmn7 hepatitis b Q9qmn7 hepatitis b Q9qmn7 hepatitis b Q9qmn7 drosophila Q9v1b9 drosophila Q9v1b2 drosophila

	T ETTOGO .)	US/133 TD OS7193 DEFITMINARY DRT 124 AA	057193:	01-NOV-1996 (TrEMBLrel.	01-OCT-2000 (TrEMBLrel.	_	_	_	OX NCBI_TAXID=666;	RN [1] BD SECTIONS RED N 3		 _		RL Biochim. Biophys. Acta 1090:139-141(1991).			RA Shi C., Zao C., Zhang J., Ma Q.;		KN 153				DR EMBL; X58785; CAA41591.1;	DR EMBL; U25679; AAC34728.1;	_	٦.	DR InterPro; IPR001835;	_	DR PRINTS; PR00772; ENTEROTOXINB.		Signal.	SIGNAL 1 21	CHAIN 22 124 CI	SQ SEQUENCE 124 AA; 13919 MW; D6BF83FFF7924EA3 CRC64;
1. 0.3 21-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	1: 0P_d1.Clas.*	2. or fund:		5: sp invertebrate:*			02				14: sp_virus:*	Drad Mo is the number of results erredicted by chance to base	and is derived by analysis of the total score distribution.	SUMMARIES	or or	Query	o. Score Match Length DB ID Description	100.0 124 2 Q57193	124 2 020033	3 100 100.0 124 2 QYKP13 QYPD13 VQYPD13 CNOI	40 1 550 10 OOTTBO	48.1 508 4 099987	46.2 428 10 09LGM2	48 45.3 392 10 Q40742	44.3 395 5 Q9NKD5	46.5 43.9 1166 3 Q9P4E0	46 43.4 293 10 049876	43.4 374 5 Q9U3M9	46 43.4 574 10 Q9SXC9	44.5 42.0 374 2 Q9PKY2	44 41.5 91 10 Q9SYF4	330 11 Q9QZL7	44 41.5 467 6 Q9N136 Q	11 P97431	19 44 41.5 1742 2 Q55583 Q55583 synechocyst

Result No.

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Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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PubMed-10907853;
                                                                                                                                                                                                                            Vibrio cholerae
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                                                   Query Match
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                                       Gaps
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NCBL_TaxID=666;
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Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misainmurhag Hoiji 35:205-210(1999).
BMBL SATI75708; AAD21360.1;
InterPro; IPR001835;
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                                                                                                                                                                                                                                                                   Yamamoto K., Do V.G., Xu M., Iida T., Miwatani T., Albert M.J.,
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                    Length 124;
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                                       Indels
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3F87B2F297953179 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                  Score 106; DB 2;
Pred. No. 2.9e-10;
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100.0%; Pred. No. 2.9e-10;
tive 0; Mismatches 0;
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                                      Mismatches
                                                                                                                                                       Created)
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Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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13871 MW;
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                                                          1 GATFQVEVPGSQHIDSQKKAI
                                      Conservative
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                 PRELIMINARY;
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                  Query Match
Best Local Similarity
Matches 21; Conserv
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Q56635;
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Q9RP15
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Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                                                                                                                                                      Gaps
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakashima K., Eguchi Y., Nakasone N.; "Characterization of an enterotoxin produced by Vibrio cholerae
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                                                                                                                              Length 124;
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Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
SEQUENCE 124 AA; 13905 MW; 23BF83FFF793E5B9 CRC64;
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HSSP; P01556; 1XTC.
InterPro; IPR001835; --
Pfam: PF01376; Enterotoxin_B; 1.

PRIMTS: PR00772; ENTEROTOXINB.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
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Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                 Score 106; DB 2;
Pred. No. 2.9e-10;
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Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                 100.0%; Sc
100.0%; Pr
tive 0;
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Matches 21; Conservative
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us-09-786-648-4.rspt

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A SABARÍ T., MACENMOTO T., Yamamoto K.;

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC ST Clone:P0437F09.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AP002539; BAAB08201.1; -.

DR EMBL; AP00441; Acyl-CoA_dh; 1.

DR PÉAN; PF00441; Acyl-CoA_dh; 1.

DR PÉAN; PF00441; Acyl-CoA_dh; 1.

DR PÉAN; PF00415; Acyl-CoA_dh; 1.

DR PÉAN; PF0043; Acyl-CoA_dh; 1.
             Sasaki T., Matsumoto T., Yamamoto K.; Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                       clone:P0041E11.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
  STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00165; UBA;
SEQUENCE 392 AA; 4
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                             Length 552;
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ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 508 AA; 58126 MW; 157FBF8F48511AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 45:327-331(1997).
-!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL: AB000450; BAA19109.1; -.
                                                                                                       Indels
TAC and BAC clones.";
DNA 7:217-221(2000).
BMBL, REPO06066; BAB01195.1; -
SEQUENCE 552 AA; 63036 MW; 740EA16CDEBB2447 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ESTS AU056822($20908).
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Last annotation update)
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                                                                            Score 52; DB 10;
Pred. No. 1.9;
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                                                                                                      2; Mismatches
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
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                                                                           Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
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147 QVEIPASMEIDEETKAI 163
                                                                                                                                5 QVEVPGSQHIDSQKKAI 21
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Q9LGM2;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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Query Match 46.2%; Score 49; DB 10; Length 428; Best Local Similarity 52.6%; Pred. No. 4.5; Matches 10; Conservative 2; Mismatches 7; Indels
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MEDILINE-97569378; PubMed-9225866;

Schultz T.F., Quatrano R.S.;

"Characterization and expression of a rice RAD23 gene.";

Plant Mol. Biol. 34:557-562(1997).

EMBL; UG5330; AAB65841.1;

HSSP; P02248; ITBE.
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                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mendel; 15760; Orysa; 2927; 15760.
InterPro; IPR000449; -.
InterPro; IPR000626; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000626; -. Pfam; PF00240; ubiquitin; 1. Pfam; PF00627; UBA; 2.
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183 TTATKVPGGWHIDGQKRWI 201
                                                                                                3 TFQVEVPGSQHIDSQKKAI 21
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Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                PRELIMINARY;
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us-09-786-648-4.rspt

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Query Match
Best Local Similarity
18, Conserve
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                InterPro;
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                                                                                                                                                                                                                                                                                                                             RESULT 11
049876
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  S W N D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R R D D R D R D D R D D R D D R D D R D D R
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AE003408; AAF448471;
FIYBase: FBGN028907; BG:DS01514.3.
                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed=10471707;
MEDLINE-99403001; PubMed=10471707;
MSbburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                     Celniker S., Rubin G.M.;
An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews D.L., Egan J.D., Mayorga M.E., Gold S.E.;
"The Ustilago maydis ubc4 and ubc5 genes encode members of a MAP
kinase cascade required for filamentous growth.";
Mol. Plant Microbe Interact. 13:781-786(2000).
-! SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AF197562; AAF86841.1; -.
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Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Length 395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l protein.
395 Aa; 43561 MW; AE4F1CC4ADD3DA73 CRC64;
           01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHEROMONE-RESPONSIVE MAPKK KINASE UBC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 5
Pred. No. 9;
2; Mismatches
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MEDLINE-20331594; PubMed-10875339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ustilago maydis (Smut fungus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.3%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.2
Matches 9; Conservative
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329 RVSVPGSTHIDADANA 344
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                                                                     BG:DS01514.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 3
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Q9P4E0
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
CLASS III CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
CHIBI OR LUPA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lupinus albus (White lupine).
Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lupinus.
                                                                                                                                                                      SMART; SM00220; S_TKC; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 1166 AA; 123298 MW; A89E0019AABD4172 CRC64;
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Regalado A.P., Vludal S., Neves A., Ricardo C.P.P.,
Rodrigues-Pousada C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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POTENTIAL.
; DB1B21728F657F2F CRC64;
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                                                                                                                                                                                                                                                                                           43.9%; Score 46.5; I
47.6%; Pred. No. 35;
Live 4; Mismatches
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InterPro; IPR000719; -.
InterPro; IPR002290; -.
Pfam; PF00069; pkinase; 1.
PRINTS; PR001308; ANTIFREEZEI.
PROSITE; PS00101; PROTEIN_KINASE_DAP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DAP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y16415; CAA76203.1; -. HSSP; P23472; 2HVM.
Mendel; 28297; Lupal;Chibl;28297.
InterPro; IPR001579; -. Pfam; PF00192; chitinase_2; 1.
PROSITE; PS01095; CHITINASE_18; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 293 AA; 31128 MW;
                                                                                                                                                                                                                                                                                                                                                                                               2 ATFQVEVP-GSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                              Query Match 43.9
Best Local Similarity 47.6
Matches 10; Conservative
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Q9U3M9;
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Q9U3M9
ID Q9U3M9
AC Q9U3M9
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C40H5.3.

White

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SEQUENCE FROM N.A.
STRAIN=MODN / NIGG;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
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Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Kremenetskaia I., Luros J., Ngan i., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Walker M.,
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome I BAC F15I1 sequence.";
submitted (Apr. 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006577; AAD257691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 374;
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47.6%; Pred. No. 5.8;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                 Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
NCBI_TaxID=83560;
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Fred. No. 22;
3; Mismatches
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01-MAY-2000 (TYEMBLREL. 13, Last sequ
01-007-2000 (TYEMBLREL. 15, Last anno
F1511.6 PROTEIN.
                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 protein.
374 AA; 41218 MW;
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                                                                                                        (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 28:1397-1
EMBL; AE002300; AAF39192.1;
                                                                                                                                                                HYPOTHETICAL PROTEIN TC0328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.0
Best Local Similarity 48.0
Matches 12; Conservative
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Matches 10; Conservative
                                                                       PRELIMINARY;
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                                                                                                        01-OCT-2000
01-OCT-2000
01-MAR-2001
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Q9SYF4;
                                                                                       09PKY2;
                                                                       Q9PKY2
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                                  RESULT
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Vysociskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysociskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Chee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano H.,
Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.
Buehhler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Parabidopsis Lhaliana chromosome 1 BAC T17H3 sequence.";
Submitted (AUG.1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AC005916, AAD45990.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                    Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                               'Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ACUUSSAC, 11
InterPro; IPPRO1382; -. Pfan: PFUSIS; BY PRO0747; 1. PRINTS; PRO0747; GLYHDRLASE47. PRINTS; PRO0747; GLYHDRLASE47. AA: 65707 MW; 4ACC456DE487EA93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        67D202886D6A7824 CRC64;
ol-mar-2000 (TrEMBLrel. 13, Created)
01-Mar-2000 (TrEMBLrel. 13, Last sequence update)
01-Mar-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
T17H3.2 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.4%; Score 46; 42.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.4%; Score 46; 58.8%; Pred. No. ;
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                                                                                                                                                                                                                                                                                            MEDLINE~99069613; PubMed~9851916;
                                                                                                                                                                                                                                                                                                                           "Genome sequence,";
investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281482; CAB03954.2; -.
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Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                NCBI_TaxID=6239;
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O9SXC9; **698XC9**

RESULT 13 69SXC9

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090ZL7

RESULT 16 Q9QZL7

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TISSUE-COLON, KIDNEY, GENOMIC DNA 129/J STRAIN (DR. J. ROSSANT);
Grossman A., Mittrucker H.W., Antonio L., Mak T.W.;
L. Submitted (CGT-1996) to the EMBL/GenBank/DDBJ databases.
R. BEMBL; 073029; ARB36714.1; -.
R. HSSP; P23906; ZIRF.
R. MGD; MGI:185911; Irf6.
R. InterPro: IPR001346; -.
R. Pfam; PF00605; IRF: 1.
R. PRINTS; PR00267; INTFRNRGFCT.
R. PRODOM; PD002355; -; 1.
R. PROSITE; PS00601; IRF: 1.
R. SMART; SM0348; IRF: 1.
C. SEQUENCE 467 AA; 53106 MW; 68CCAA90680FEDC8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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  Length 467;
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
U-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INTERFERON REGULATORY FACTOR 6.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
NYPOTHETICAL 179.7 KDA PROTEIN.
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9
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Pred. No. 35;
6; Mismatches
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DB
35;
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                                                        Mismatches
  Score 44;
Pred. No. 3
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  41.5%;
41.2%;
                                                                                                                                             273 QVKFPGPEHITNEKQKL 289
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                                                                                                        5 QVEVPGSQHIDSQKKAI 21
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                            Best_Local Similarity 41.2
Matches 7; Conservative
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41.5
Best Local Similarity 41.2
Matches 7; Conservative
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STRAIN-BALB/C;
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     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             055583;
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                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sands A., Mak T.W.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR177668; ARF00915.1; -.
INTERPROPREDIATE.
InterPro; IPR001346; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SMO0348; IRF; 1.
SEQUENCE 467 AA; 52970 MW; 21E04F749844D88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 AA; 37355 MW; EB02EC8B751CBD7D CRC64;
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0LMAR-2001 (TrEMBLrel. 16, Last annotation update)
INTERFERON REGULATORY FACTOR 6.
Ovis aries (Sheep).
                                                                                                                                                                                            330 AA
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                                                                                                                                                                                                                                                  Created)
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PRINTS, PRODGS7; INTFRINEGFCT.
PROSITE; PS00601; IRF; 1.
SMART; SM00348; IRF; 1.
  1 GATFQVEVPGSQHIDSQKKAI 21
                               58 GKTFNLEVKGSEIIQQVKNMI 78
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PRINTS, PR00267; INTERNEGECT.
PRODOM; PD002355; -; 1.
PROSITE; PS00601; IRF; 1.
                                                                                                                                                                                                                      09QZL7;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
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Best Local Similarity
7; Conserve
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STRAIN-129/J;
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IRF6.
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09N136 Q9N136,

RESULT 17 Q9N136

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233 GRPFIPEIPGSEHAIDS 249
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                                                   RESULT 21
Q43098
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                                                                          Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta;
Synechocystis sp. strain PCC6803, I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A); TISSUE-FRUIT;
Cassol T., Adams D.O.;
Submitted (AUG-1997) to the EMBL/Genbank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
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Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis
NCBL_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 565;
                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 1742;
Pred. No. 1.5e+02;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                       InterPro; IPR002048; -.
PROSTIE: PS00118; EF_HAND; UNKNOWN_4.
Hypothetical protein.
SEQUENCE 1742 Aa; 179710 MW; 56C815A887D30B82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAD; Flavoprotein; Oxidoreductase; Redox-active center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTATHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.0%; Score 43.5; DB 10;
58.8%; Pred. No. 52;
iive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           565 AA
                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                     MEDLINE=97061201; PubMed=8905231;
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Mendel; 26381; Vitvi;1190;26381.
InterPro; IPR000103; -.
                                                                                                                                                                                                                                                                                                                                                                            121 GGTFSIDVPGSALVADPDRTI 141
                                                                                                                                                                                                                                                                                                                                                             1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00070; pyr_redox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF019907; AAB70837.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001100; -. InterPro; IPR001327; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vitis vinifera (Grape).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  565 AA;
                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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022511
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1 GATFQVEVPGSQH-IDS 16

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Gaps
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-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
HYDROLASES).
                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
MEDLINE-98249626; PubMed=9588027;
Baba M., Teramoto T.;
"cDNA cloning, gene expression and secretion of chitinase in winged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
                                                                                                                                   Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
Eukaryota; Viridiplantue; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Paplilonoideae; Psophocarpus.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 10; Length 298; Pred. No. 31; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
EMBL; AL139794; CAC22649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001579; -.
Pfam; PF00192; Chitinase_2; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Glycosidase; Hydrolase.
SEQUENCE 298 AA; 31557 MW; 675D1379D46424E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CHITINASE (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 AA
298 AA
                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 GVDFDIESGGSNHYDDLARAL 166
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Best Local Similarity 38.1%;
Matches 8; Conservative
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                                      01,
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PRELIMINARY;
                                      01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
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Leishmania major.
                                                                                                                                                                                                                       NCBI_TaxID=3891;
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Search completed: July 16, 2001, 16:43:38
Job time: 472 sec
         NCBI_TaxID=542;
                                                                             STRAIN-ZM4;
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Q9LY67
           SO REPRESENTATION OF THE PROPERTY OF THE PROPE
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EMBL; AE000872; AAB85482.1;
                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09F5L7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRNA GANINE TRANSGLYCOSYLASE.
Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
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Pred. No. 39;
6; Mismatches 6; Indels
                                                                                                                                          5; Length 356
                                                                                                                                                                                      5; Indels
                                                                        356 AA; 39755 MW; FE5C8A120287F299 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 16, Last annotation update)
SENSORY TRANSDUCTION HISTIDINE KINASE.
MTH985.
                                                                                                                                          Score 43; DB 5
Pred. No. 38;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             365 AA.
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                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPR002123; -
Pfam; PF01553; Acyltransferase; 1.
Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00512; signal; 1.
Pfam; PF00989; PAS; 1.
SMART; SM00387; HATPASe_c; 1.
SEQUENCE 365 AA; 41615 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.6%;
                                                                                                                                          40.6%;
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49 AIFLVKIPGGELVDANRSA 67
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Best Local Similarity 38.9'
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.6
Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                        SEQUENCE
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09F5L7
1D 09F5L7
AC 09F5L7
DT 01-MAR
DT 01-MAR
DT 01-MAR
DF TRNA G
OS Zymomo
OC Bacter
OC 2ymomo
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                                                                   "Sequence analysis of 4486 fosmid clone of Zymomonas mobilis ZM4.";
Submitted (COT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF313764; AAG29862.1; - SEQUENCE 399 AA: 44287 WW; 75CEF229E70F94A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Schaefer M., Mewes H.W., Rudd Heger M., Mueller Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                        Length 399;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALLG3818; CAB87801.1; -
InterPro; IPR001752; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00129; KISC; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 439 AA; 49028 MW; 9BD55085A1966D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 AA
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PRINTS; PR00380; KINESINHEAVY.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                                                                                                                  Pred. No. 43;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                        40.6%; Score 43; 38.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINESIN HEAVY CHAIN-LIKE PROTEIN. MAA21_110.
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                                                                                                                                                                                           Query Match
Best Local Similarity 38.1.,
Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 GKTYSMEGPGIQDCDEHNKGL
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Matches 8; Conservative
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                                              Ahn J.Y., Kang H.S.;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	
OM protein - pro	OM protein - protein search, using sw model	
Run on:	July 16, 2001, 16:35:41; Search time 56.06 Seconds (without alignments) 22.710 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-786-648-5 107 1 GETFQVEVPGSQHIDSQKKAI 21	
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	٠
Searched:	412676 seqs, 60623988 residues	
Total number of	Total number of hits satisfying chosen parameters: 412676	
Minimum DB seq le Maximum DB seq le	Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	

A_Geneseq_0601:*

| SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSB/gcgdata/geneseqp/GAA1981.DAT:*
| SIDSB/gcgdata/geneseqp/AA1981.DAT:*
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| SIDSB/gcgdata/geneseqp/geneseqp/AA1980.DAT:*
| SIDSB/gcgdata/geneseqp/geneseqp/AA1990.DAT:*
| SIDSB/gcgdata/geneseqp/AA1990.DAT:*
| SIDSB/gcgdata/geneseqp/geneseqp/AA1990.DAT:*
| SIDSB/gcgdata/geneseqf/geneseqp/AA1990.DAT:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	E. coli heat labil	ADP-ribosylating t	Escherichia colí v	E. coli heat-labil	Heat labile toxin	E coli verotoxin-1	Recombinant exotox	Recombinant exotox	Recombinant exotox	Recombinant exotox	Labile toxin (LT-B
	ID	AAY87463	AAR72545	AAY41816	AAW95226	AAY68365	AAB66239	AAB73241	AAB73242	AAB73243	AAB73244	AAY01300
	DB	21	16	20	20	21	22	22	22	22	22	20
	Query Match Length DB	21	93	93	93	93	93	134	142	155	163	371
ф	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	107	107	107	107	107	107	101	107	107	107	107
	Result No.		7	m	4	S	9	7	00	6	10	11

C. jejuni flagelli	Cholera toxin B/en	Synthetic cholera	Heat labile entero	Cholera toxin B su	Cholera toxin B su	Amino acid sequenc	Cholera Toxin B-su	B subunit of the h	Cholera toxin B su	Amino acid sequenc	Plant-optimized E.	LTB-CTB fusion pro	Sequence of LT-B-M	LTB-CTP fusion pro	HSV-1 antigen/heat	Sequence of sub-un	Plant-optimized V.	GtfB.1/CTB chimeri	Network polymer wh	B subunit of CT.	Adhesin/V.cholerae	Helicobacter pylor	Helicobacter pylor	Network polymer wh	Sequence of amino	Adhesin/CTXA2B chi	Sequence of amino	CTP3 epitope of th	Cholera toxin B an	Residues 50-64 of	Cholera toxin B/en	Cholera toxin B su	Bovine rotavirus V
20 AAW67443	21 AAY87462	17 AAW04857	17 AAR94939	17 AAW06606	17 AAW06607	19 AAW80808	11 AAR04163	10 AAP93561	17 AAW06605	19 AAW59770	21 AAY96652	11 AAR04825	15 AAR50227	20 AAW94082	12 AAR11272	6 AAP50340	21 AAY96872	12 AAR12630	6 AAP50439		19 AAW74466	19 AAW80599		6 AAP50436	4 AAP30600	20 AAY32094	4 AAP30265	10 AAP93498	16 AAR85125	16 AAR76748		21 AAB15525	21 AAB15526
371	21	103	103	103	103	103	118	124	124	124	124	131	138	170	405	103	124	126	41	124	461	749	1338	46	47	461	26	15	15	23	12	, 15	15
100.0	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	91.6	88.8	88.8	87.9	83.2		83.2	83.2	82.2	ä	9.9/	74.8	71.0	71.0	71.0		57.0	57.0
107	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	86	95	95	94	89	89	. 89	89	88	87.5	82	80	16	92	97	62	61	61
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43:	44	45

ALIGNMENTS

RESULT

Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea. E. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5. Ą 21 AAY87463 standard; peptide; 99WO-GB02970. 98GB-0019484 03-JUL-2000 (first entry) Williams NA, Hirst TR; (UYBR-) UNIV BRISTOL. WPI; 2000-256943/22. Escherichia coli. WO200014114-A1. 07-SEP-1998; 07-SEP-1999; 16-MAR-2000. AAY87463; AAY87463

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

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Disclosure; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                              AAY41816;
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                    RESULT
AAY41816
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                                                                                                                                                                                                                                                                                                        g
                       The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubjuditous. GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is ribosyltransferase activity, while the B subunits (RtxB and CtxB) robsyltransferase activity, while the B subunits (EtxB and CtxB) and crabsyltransferase activity, while the B subunits (EtxB and CtxB) and crabsyltransferase activity, while the B subunits (EtxB and CtxB) and crabsyltransferase activity, while the B subunits (EtxB and CtxB) and crabsyltransferase activity, while the B subunits (EtxB and CtxB) and crabsyltransferase of the effects of Etx and Ctx, it has been found that certain through GM-1 Inding 1 The peptides of the invention are fragments of the crabsyltransferase and in menomodulation of adjuvant.

They may also be used as an inhibitor for toxin-induced diarrhoea.

Therefore, the peptides may be used in the production of a composition of mmune disorder and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAV87460-Y87463
                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes with
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loosmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 107; DB 21;
Pred. No. 1.4e-11;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP-ribosylating toxin (verotoxin-1 B-subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В,
Disclosure; Page 15; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR72545 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GD, Cockle SA, Hazes
Read RJ, Stein PE;
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                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHIDSQKKAI 21
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94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                    particularly preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-132623/18
                                                                                                                                                                                                                                                                                                                                                                 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                  Sequence
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A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises: (1) identification of at least one amino acid (aa) residue of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structure of the pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                          Gaps
                ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
AAR72540-R72545 are structurally equivalent B-subunits from three
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                                                                                                                                                                                                                               Length 93;
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method for producing modified pertussis holotoxin
                                                                                                                                                                                                                                 100.0%; Score 107; DB 16;
100.0%; Pred. No. 8.1e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli verotoxin-1 B-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY41816 standard; peptide; 93 AA
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93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 5; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CONN-) CONNAUGHT LAB (UYAL-) UNIV ALBERTA.
                                                                                                                                    pertussis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-579908/49.
                                                                                                                                                                          93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1994;
24-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5965385-A.
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holotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin B-subunit peptide used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                  Length 93;
                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli heat-labile toxin (LT) beta-subunit sequence.
                                                                                                                                                                                                      20;
                                                                                                                                                                                                  Score 107; DB 20;
Pred. No. 8.1e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iD, Cockle SA, Hazes B,
Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                     AAW95226 standard; peptide; 93 AA.
                                                                                                                                                                                                  100.0%; Sc
100.0%; Pr
tive 0;
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94US-0251121
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                                                                                                                                                                                                                   Local Similarity 100.
Les 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat-labile; LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Armstrong GD,
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                                                                                                              invention
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                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW95226;
                                                                                                                                                                                                    Query Match
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Matches
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The complexed with a polysaccharide molecule capable of forming a complexed with a polysaccharide molecule capable of forming a complex with the holotoxin: The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAX68340 to AAX68385 represent peptides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                              Gaps
toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present sequence represents the beta-subunit of LT toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crystalline form of isolated pertussis holotoxin useful in studying proteins which have functional resemblance -
                                                                                                                                            ö
                                                                                                              93;
                                                                                                            Length
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein MH,
                                                                                                              20;
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                                                                                                           100.0%; Score 107; DB 20; 100.0%; Pred. No. 8.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cockle SA, Loosmore S,
                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Heat labile toxin B subunit SEQ ID NO:26.
                                                                                                                                                                                                                                                                                         AAY68365 standard; Peptide; 93 AA.
                                                                                                                100.0%; Fr. 0;
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93US-0110947.
94US-0251121.
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                                                                                                                                                                              1 GETFQVEVPGSQHIDSQKKAI
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                                                                                                                                            21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-136703/12.
                                                                                                            Query Match
Best Local Similarity
Matches 21; Conserv
                                                               93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 AA;
                                                                                                                                                                                                                                                                                                                                                        17-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6018022-A.
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Hazes B,
                                                                                                                                                                                                                                                                                                                          AAY68365;
                                                                 Sequence
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                                                                                                                                                                                                                                                                           AAY683
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(first entry)

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Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                            Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                Recombinant exotoxin protein variant LTBpL.
 AAB73241 standard; Protein; 134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 9; 57pp; English.
                                                                                                                                                                                                                                                                        18-AUG-2000; 2000WO-US22715.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-211103/21.
N-PSDB; AAF75712.
                                                                                                                                                                                                                                                                                                                                    (AGRI-) AGRIVAX INC
                                                                                                                                                                                                           WO200111960-A1
                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                      18-AUG-1999;
                                                               14-MAY-2001
                                                                                                                                                                                                                                         22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                     Welter LM;
                                 AAB73241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection
                                                                                                                                                                                                                                                                                                   Pertussis toxin, crystal structure, whooping cough, biological activity, lymphocytosis-promoting factor, histamine-sensitising factor; islet-activating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, call binding or enzyme activity of PT and modifying identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein MH, Armstrong GD;
                                  Gaps
                                 ;
0
   Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 93;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 107; DB 22;
100.0%; Pred. No. 8.1e-11;
ive 0; Mismatches 0;
 DB 21;
Score 107; DB 21;
Pred. No. 8.1e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loosmore S,
                                                                                                                                                                                                                                                                      E coli verotoxin-1 B subunit SEQ ID NO: 26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cockle SA, Oomen RP,
Stein PE;
                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 5; 41pp; English
                                                                                                                                                                           AAB66239 standard; Protein; 93
100.0%;
                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0292968.
93US-0110947.
94US-0251121.
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                                                                                 1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                       (first entry)
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              Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by Bordetella pertussis.
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Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                  Escherichia coll
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24-AUG-1993;
31-MAY-1994;
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Query Match
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The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-lable enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid encodes an antigen to which the immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 107; DB 22; 100.0%; Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant exotoxin protein variant LTBpLh.
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                               134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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Gaps

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1 GETFQVEVPGSQHIDSQKKAI 21

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                                                                                                                                                                         The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-lable enterotoxin (LT) of Escharichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                           Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif an exotoxin and a nucleic acid affinity domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 107; DB 22;
100.0%; Pred. No. 1.5e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant exotoxin protein variant LTB-Ph.
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                                                                                                                                           Example 1; Fig 11; 57pp; English.
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Best Local Similarity 100.
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WPI; 2001-211103/21.
N-PSDB; AAF75714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                155 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid concodes an antigen to which the immune response when the fuclic colid encodes an antigen to which the immune response is desired, expression of a protein in a subject, by administering a composition comprising the protein variant.
                                                                                                                                                                                                                                                                                                                        Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
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100.0%; Score 107; DB 22;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant exotoxin protein variant LTB-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73243 standard; Protein; 155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 10; 57pp; English
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                                                                                                   18-AUG-2000; 2000WO-US22715
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                                                                                                                                                                                                                                                             WPI; 2001-211103/21.
N-PSDB; AAF75713.
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                                                                                                                                                                                 (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 AA;
                WO200111960-A1
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                                                                                                                                           18-AUG-1999;
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                                                                                                                                                                                                                       Welter LM;
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Sequence

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AAB73243 RESULT

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This represents a fusion protein that comprises the B subunit of labile toxin (LT-B) of E. coli and part of the flagellin (flaA) protein of C. jejuni. The fusion protein is amtigenic and is useful for decreasing colonisation in chickens by Campylobacter species. The labile toxin B-subunit component of the fusion protein (i) binds to ganglioside GMI component to the mucosal surface of eukaryotic cells, delivering the antigenic flagellin component to the mucosal surface, resulting in an immune response against campylobacter jejuni reducing colonization by the organism; and (ii) has an adjuvant effect on immunoglobulin A secretion. The fusion protein expressed by the recombinant gene is relatively simple to produce and purify, can be produced in large quantities and can be used for vaccination without any further treatment other than purification.
was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein; labile toxin B subunit; LT-B; E. coli; flagellin; flaA; C. jejuni; antigenic; colonisation; chicken; Campylobacter; vaccine; immune response; ganglioside GMI; immunoglobulin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                          Length 163;
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                                                                                                                                                                                                                                                                                                                                                                          Score 107; DB 22;
Pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 16-20; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY01300 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                      100.0%; Sc
100.0%; Pr
live 0;
                                                                                                                                                                                                            the protein variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
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Escherichia coli.
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                                                                                                                                                                                                                                                                       163 AA;
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                                                                                                                                                                                                            comprising
                                                                                                                                                                                                                                                                              Seguence
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371 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a recombinant fusion protein consisting of the Campylobacter jejuni flagellin protein (flaA) fused to the Escherichia coli B subunit of the labile toxin (LT-B). The fusion protein is antigenic and when administered in vaccines decreases colonisation of chickens by Campylobacter species. The LT-B component serves to deliver the flagellin antigen to mucosal surfaces and also has an adjuvant effect
                                                                                                                                                                                                                                                           Recombinant; fusion protein; flagellin; flaA; labile toxin; antigen; vaccine; colonisation; chicken; mucosal surface; adjuvant; secretion; immunoglobulin A.
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant fusion protein of Campylobacter jejuni flagellin protein and Escherichia coli labile toxin – useful in vaccines to reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
 Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 371;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Escherichia coli labile toxin - useful in vac
colonisation of chickens by Campylobacter species
100.0%; Score 107; DB 20;
100.0%; Pred. No. 4.2e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 107; DB 20;
100.0%; Pred. No. 4.2e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                   C. jejuni flagellin/E. coli LT-B fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 17-20; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY87462 standard; peptide; 21 AA.
    100.08; Pr.
                                                                                                                                                                                                                                                                                                                     Chimeric - Campylobacter jejuni.
Chimeric - Escherichia coli.
                                                                                                                                                  AAW67443 standard; Protein; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on immunoglobulin A secretion.
                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0829026.
                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0150305.
97US-0829026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meinersmann RJ;
                                                                     49 getfqvevpgsghidsgkkai
                                                      1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GETFOVEVPGSOHIDSOKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USDA ) US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-023536/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 21; Conserv
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV34380.
                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1997;
                                                                                                                                                                                                         02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                             US5837825-A
               Best Local Sim
Matches 21;
                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khoury CA,
                                                                                                                                                                              AAW67443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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AAY87462
ID AAY8
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Recombinant constructs comprising a promoter functional in Bordetella leader sequence for a heterologous gene or a non-construct and bordetella leaders requence for secretion of a gene product which may or may not be of Bordetella, immunogens, allergens, enzymes or may not be of Bordetella, immunogens, allergens, enzyme in Bordetella of enzymes, antigens, immunoglobulins or their fragments, toxins, mammalian proteins, structural proteins or receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, fha promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the constructs are selected from the cholera toxin B leader (CTB-L), the pertussis toxin subunit si leader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from a leader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from a leader (CTB-L), and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from an ovel synthetic cholera toxin B gene (ctb) and the hmml and hmw2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and
                                                                                                                                                                               structural protein; receptor; heterologous gene; leader; promoter.
                                                                                                                          cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin;
                                                                                                       Bordetella pertussis; whooping cough; recombinant construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 17;
Pred. No. 9.7e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yacoob RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR94939 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Figure 1; 61pp; English.
                                                     Synthetic cholera toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.48;
95.28;
                                                                                                                                                                                                                                                                                                                                                                                   96WO-CA00107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loosmore SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-425088/42.
N-PSDB; AAT38038.
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Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene of interest
                                                                                                                                                                                                                                                                            WO9626282-A1
                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1995;
21-FEB-1997
                                                                                                                                                                                                                                                                                                                                 29-AUG-1996.
                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR94939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
AAR94939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera coxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Exx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) acilitate the entry of subunit A into the host cell via the binding and facilitate the entry of Subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated for some of the toxins, such as immunomodulation are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as corrected and in mediated diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460 being reperted. Particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                               Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                            Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 21;
Pred. No. 1.5e-10;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15; 62pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-0019484
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                                               03-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams NA, Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-256943/22.
                                                                                                                                                                                                                                                    Vibrio cholerae.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                            WO200014114-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1999;
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Zealey GR;

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Gaps

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Indels

Sequence

Heat labile enterotoxin B subunit (LT-B) E.coli.

AAW04857;

RESULT 14

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Length 103;

substitution

/label=

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02-MAY-1996;
                                                                                                                          05-MAY-1995;
                                                             WO9634893-A1
                                                                                  07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAW06605)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                  A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjivants. The method provides an inexpensive production and delivery system for such antigens on animals. This is the LT-B Escherichia coli toxin subunit and its
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat labile, tolerant, stable, hybrid, cholera toxin B subunit, CTB; heat labile enterotoxin B subunit, LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                coding sequence was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B.subunit) or optionally LT-A or CT-A.
                                                                                                                                                                                                                  Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
 Toxin; subunit; vaccine; transgenic plant; immunogen; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 17; Length 103;
Pred. No. 9.7e-10;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= substitution
/note= "wild-type Thr replaced by Ala"
Misc-difference 94
                                                                                                                                                                  Mason HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Vibrio cholerae.
- Enterotoxigenic Escherichia Coli.
                                                                                                                                                                                                                                                 Disclosure; Page 100-101; 130pp; English.
                                                                                                                                                                 Clements JD, Hag TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW06606 standard; Protein; 103 AA.
                                                                                                                                  (TULA ) TULANE EDUCATIONAL FUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 gatfqvevpgsqhidsqkkai 65
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                                                                                                                                                                                                                                                                                                                                                                                                                         94.48;
95.28;
                                                                                           95WO-US13376.
                                                                                                               94US-0328716
                                                                                                                                                                                  WPI; 1996-230602/23.
N-PSDB; AAT18799, AAT18800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.2
Matches 20; Conservative
         adjuvant; immunisation
                                                                                                                                                                                                                                                                                                                                                                                          103 AA;
                             Escherichia coli.
                                                  WO9612801-A1
                                                                                          24-OCT-1995;
                                                                                                               24-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1997
                                                                                                                                                                 Arntzen CJ,
                                                                      02-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW06606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW06606
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AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding aa from cat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea cand vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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/note= "wild-type His replaced by Asn"
                                                          /label= substitution
/note= "wild-type Ala replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 17;
Pred. No. 9.7e-10;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic Escherichia Coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW06607 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page -; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.4%;
llarity 95.2%;
Conservative (
                                                                                                                                                                                                                                                                                       96WO-SE00570.
                                                                                                                                                                                                                                                                                                                                                     95SE-0001682.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                               (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT43576
                                   Misc-difference
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cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the cholera toxin B subunit used in the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as an mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it enables the possibility for commercial mucosal adjuvants for use in humans, since these are more effective and safer than vaccines
                                                                                                                                                                                                                                                                                                      New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered with an antigen to birds and mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..11
/*label= signal peptide
/*note= absent from mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 19;
Pred. No. 9.7e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                          Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18..18
/*label= His or Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR04163 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1B; 43pp; English.
                                                                                                                                                                                                                                        Takeda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  administered subcutaneously
                                                          98WO-US06725
                                                                                           97US-0043410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89WO-0000495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 gatfqvevpgsqhidsqkkai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera Toxin B-subunit.
                                                                                                                           (KIYO/) KIYONO H.
(MCGH/) MCGHEE J R.
(TAKE/) TAKEDA Y.
(UARR-) UAB RES FOUND.
(TAMA/) YAMAMOTO S.
                                                                                                                                                                                                                                        Mcghee JR,
                                                                                                                                                                                                                                                                          WPI; 1998-594478/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
misc_difference
                                                          03-APR-1998;
                                                                                           04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-1989;
                      15-0CT-1998.
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                                                                                                                                                                                                                                        Kiyono H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic lilness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Location/Qualifiers
1..25
//label= substitution
//note= "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the wild type chorela toxin B subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 17;
Pred. No. 9.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW80808 standard; protein; 103 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page -; 32pp; English.
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Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                               Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                           (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 AA;
                      Misc-difference 1.
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT43577
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                                                                                                                                                WO9634893-A1
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                                                                                                                                                                                                                   02-MAY-1996;
                                                                                                                                                                                                                                                       05-MAY-1995;
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                                                                                                                                                                                  07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW06605).
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RESULT 18 AAW80808

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Length 103; 1; Indels

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In the patent, the DNA encoding LT-B is expressed as part of a fusion protein with an epitope of a malaria parasite, eg Region I or Region II or a repeat region of circumsporozoite protein antigen (CS) (AAP93560) from Plasmodium berghel. Pref. the fusion gene is inserted into attenuated Salmonella enteriditis under the left promoter control of lambda. Such bacteria can multiply in the host without causing disease or disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be multivalent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholera toxin B subunit, used for hybrid immunogenic toxin production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW06605 is the full (including the signal peptide) length cholera toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amino acids (aa) of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                           Length 124;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                        Score 101; DB 10;
Pred. No. 1.2e-09;
); Mismatches 1;
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/label= sig_peptide
22..124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06605 standard; Protein; 124 AA.
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                                                                                                                                                                                                                                                           94.4%;
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| |||||||||||||||||||||||||||||gatfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 95.2
Matches 20; Conservative
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N-PSDB; AAT43575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                         124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9634893-A1
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                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW06605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
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                                                                                                                                                                                                                                                                        Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B subunit of the heat-labile enterotoxin (LT-B) derived from E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malari
circumsporozoite protein; fusion protein; live recombinant vaccine;
Salmonella; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                               New hybrid protein, useful in vaccines \boldsymbol{\cdot} contains cholera toxin \boldsymbol{b} subunit and heterologous IgA active
                                                                                                                                                                                                                                                                                                                                                                                                    Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Live recombinant vaccine for malaria - comprising attenuated entero-invasive bacterium contg, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 94.4%; Score 101; DB 11;
95.2%; Pred. No. 1.1e-09;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pillai S, Hockmeyer WT;
                                       (UYLI-) L'UNIVERSITE DE L'ETAT A LIEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..22
/note="Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding epitope of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP93561 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 3; p. 3/17; 105pp; English
                                                                             Martial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                       Disclosure; ; pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brey RN, Majarian WR,
                                                                             Renard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-114399/15.
N-PSDB; AAN90747.
                                                                                                            WPI; 1990-132273/17
                                                                                                                                                                                                       antigenic sequence.
                                                                                                                                                                                                                                                                                                                                              118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                               N-NSDB; 004046
     27-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1988;
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                                                                         L'Hoir C,
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP93561;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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888888888888

95.2%;

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AAW06606 and AAW06607. The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (LTB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antigenic peptide is an inhibin fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducing an immune response against the antigenic peptide. Vaccines are particularly administered orally, e.g. fusion protein is expressed in edible plants or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-subunit of heat labile enterotoxin; LTB; fusion protein; vaccine; immunogen; antigen; inhibin; fertility; follicle stimulating hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding fusion of antigenic peptide and enterotoxin sub-unit - useful as vaccinating immunogen, particularly for increasing animal fertility by inducing antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                 94.4%; Score 101; DB 17; Length 124; 95.2%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW59770 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of E. coli LTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSH; sperm; ova; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 9; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0747410.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bagdasarian M, Ireland J;
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 95.2 les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-297947/26.
N-PSDB; AAV41573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA;
                                                                                                                                                                                                                                                         124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9821344-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1996;
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                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW59770;
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibin
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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Length 124;

DB 19;

94.4%; Score 101;

Query Match

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This synthetic Escherichia coli heat-labile toxin (LT) B subunit (LT-B) is encoded by a plant-codon optimized cDNA. The cDNA sequence contains plant-preferred codons and eliminates sequence motific associated with spurious mRNA processing. The second codon is changed from AAT encoding ABD to GTG encoding Val, in order to create a NGOI restriction site at the 5' end. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or a polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially cral vaccines in transgenic plants for the prophylactic or therapeutic contact against E. Coli or V. cholerae. The mutant polypeptides are
                              ó
                                                                                                                                                                                                                                                                                   Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                              ö
                              Indels
                                                                                                                                                                                                                                                              Plant-optimized E. coli heat labile toxin B subunit.
Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                        22..124
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                       /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOYC-) BOYCE THOMPSON INST PLANT RES. (MASO/) MASON H S. (ARNI/) ARNIZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                   AAY96652 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 5A-B; 103pp; English.
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                                                                            66 gatfqvevpgsqhidsqkkai
                                                           1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                  (first entry)
            Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA51156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mason HS,
                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                   AAY96652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                        AAY96652
                                                                                       qq
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Gaps

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Indels

Score 101; DB 11; Pred. No. 1.3e-09;); Mismatches 1;

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94.4%; 95.2%;

21

Length 131;

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This allows the use of a strategically placed EcoRI site just upstream
         of the RBS on the LTB gene for the insertion of a strong tac promoter for the expression of CTB. The protein can be used as vaccines, diagnostic reagents and receptor-blocking agents for prophylaxis of cholera and E.coli diarrhoea.
                                                                                                                         GETFQVEVPGSQHIDSQKKAI
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-118162/14.
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                     Ŗ,
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                                                    131
                                                                                                                                                                                                                                                                                                                              15-SEP-1993;
                                                                                                                                                                                                                                                                                                                                               16-SEP-1992;
                                                                                                                                                                                                               09-OCT-1994
                                                                                                                                                                                                                                                                                             WO9406465-A
                                                                                                                                                                                                                                                                                                             31-MAR-1994
                                                                                                20;
                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                              AAR50227;
                                                     Sequence
                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Dale JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                           25
                                                                                                                                  73
                                                                                               Matches
                                                                                                                                                                      AAR50227
                                                                                                                                                             RESULT
888888
                                                                                                                                 Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression of binding sub-unit protein of cholera toxin - using foreign promoter with no V cholera DNA between promoter and ribosome binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is produced by genetically fusing the leader sequence for E.coli heat-labile enterotoxin subunit (LTB) by its 3' SacI end to the 5' NdeI end of the cholera toxin subunit (CTB) via a synthetc linker.
                   Gaps
                  ö
Score 101; DB 21; Length 124; Pred. No. 1.2e-09;
                  Indels
                                                                                                                                                                                                                                                                                                    24..25
/label=cleavage to release mature CTB
                                                                                                                                                                                                                                                                                                                              CTB
                                                                                                                                                                                                                                                                   25..28
/label=part of CTB leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                  'label=D = N in classical 569B CTB
                                                                                                                                                                                                                                                                                                                                                                                                                    = N in classical 569 CTB
                                                                                                                                                                                                                                        /label=first AA of mature LTB
                                                                                                                                                                                                                                                 23..24
/label-AAs encoded by linker
                                                                                                                                                                                                                                                                                                                               release
       Pred. No. 1.26); Mismatches
                                                                                                                                                                                                                1..21
/label=LTB leader sequence
                                                                                                                                                                                                                                                                                                                                                                 Tor CTB
                                                                                                                                                                                                                                                                                                                                               Tor CTB
                                                                                                                                                                                                                                                                                                                                                                                 Tor CTB
                                                                                                                                                                     Cholera toxin; diarrhoea; enterotoxin.
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      5..26
Tabel=cleavage to
                                                                                               AAR04825 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                               label-H - Y in El
                                                                                                                                                                                                                                                                                                                                                                label=T = I in El
                                                                                                                                                                                                                                                                                                                                                                                 'label=G = S in El
                                                                                                                                                                                                                                                                                             'label-mature CTB
                 ö
94.48;
                                  1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                     Vibrio cholreae serogroup 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89EP-0850295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88SE-0003291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89NO-0003702
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; ; p; English.
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    /label=D
                                                                                                                                                  LTB-CTB fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sanches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-149724/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOLM/) HOLMGREN J.
         Local Similarity
                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR04825
                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                                     Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1988;
15-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1989;
                                                                                                                                  25-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holmgren J,
                                                                                                                                                                                                                                                                                                                                                                                                                                     EP368819-A,
Query Match
                                                                                                                AAR04825
                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                  Peptide
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          Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant hybrid streptococcal M protein antigen(s) - which elicit opsonic antibodies without eliciting cross-reactive antibodies to mammalian heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    B subunit; labile toxin; M protein; fusion protein; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group A streptococci; rheumatic fever; pharyngitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 15;
Pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies against type 24 streptococci.
                                                                                                                                                                                                                                                                                                                                                                        Sequence of LT-B-M24 hybrid molecule.
                                                                                                                                                                        AA.
                                                                                                                                                                 AAR50227 standard; Protein; 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYTE-) UNIV TENNESSEE RES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 1; 45pp; English.
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0945860.
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                                                                                                                                                                                                                                                                                                      (first entry)
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Mon Jul 16 16:58:12 2001

Qy Dp

Search completed: July 16, 2001, 16:35:42 Job time: 206 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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July 16, 2001, 16:32:16 ; Search time 56.06 Seconds (without alignments) 7.570 Million cell updates/sec OM protein - protein search, using sw model Run on:

Title:

US-09-786-648-2 39 1 EVPGSQH 7 Perfect score: Sedneuce:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

412676 seqs, 60623988 residues Searched:

412676

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:* /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:* A_Geneseq_0601:* :. /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:* :. /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* :. /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT: /SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT: /SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT: /SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT: /SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1995

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

SUMMARIES

Description	Cholera toxin B/en	Cholera toxin B/en	Cholera toxin B/en	CTP3 epitope of th	Cholera toxin B an	Cholera toxin B/en	E. coli heat labil	Residues 50-64 of	Sequence of amino	Network polymer wh	Network polymer wh
CI	AAY87460	AAY87464	AAY87461	AAP93498	AAR85125	AAY87462	AAY87463	AAR76748	AAP30265	AAP50439	AAP50436
DB :	21	21	21	10	16	21		16	4	9	9
Query Match Length DB	7	6 0	12	15	15	21	21	23	26	41	46
	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	39	39	39	39	39	39	39	39	39	39	39
Result No.	1	7	æ	4	2	9	7	80	6	10	11

Sequence of amino ADP-ribosylating t Escherichia coll v E. coll heat-labil Heat labile toxin E cols verotoxin-1 Sequence of sub-un Synthetic cholera Heat labile entero Cholera toxin B su Amino acid sequenc Plant-optimized E. Plant-optimized V. GffB J/CTB Chimeri LTB-CTB fusion pro Recombinant exotox	Labile toxin (LT-B C. jejuni flagelli HSV-1 antigen/heat Human secreted pro B subunit of CT. Human secreted pro Human heart lecith Murine lecithin-ch
AAP30600 AAR7245 AAR95286 AAW95226 AAX68365 AAR56239 AAR56239 AAR94939 AAR94939 AAR94939 AAR94939 AAR96607 AAW06607 AAW06607 AAW06605 AAW59770 AAW59770 AAR53241	A
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447 933 933 933 933 933 933 933 933 933 93	371 371 371 405 51 124 318 379
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ALIGNMENTS

RESULT AAY87460

AAY87460 standard; peptide; 7 AA.

AAY87460; ACCOS NAME OF A PART OF A PACT OF A

03-JUL-2000 (first entry)

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:2.

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Vibrio cholerae

Escherichia coli.

WO200014114-A1.

16-MAR-2000.

99WO-GB02970 07-SEP-1999; 98GB-0019484 07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Hirst TR; Williams NA,

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

Claim 1; Page 13; 62pp; English.

us-09-786-648-

The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholers toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous GW-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, while the B subunits (EtxB and CtxB) ribosyltransferase activity, while the B subunits (EtxB and CtxB) across-linking of GW-1 receptors. Although GW-1 binding is responsible. Cor some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GW-1 binding; The peptides of the invention are fragments of the beta-4-alpha-2 loop of EtxB and CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GW-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAVB7460-YB7463

Sequence

ó Gaps ö 100.0%; Score 39; DB 21; Length 7; 100.0%; Pred. No. 3.4e+05; Live 0; Mismatches 0; Indels 7; Conservative Query Match Best Local Similarity Matches 7; Conserv

1 EVPGSQH 7

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1 evpgsgh 7

g

AAY87464 standard; peptide; 8 AA. AAY87464

03-JUL-2000 AAY87464;

(first entry)

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Cholera toxin B/enterotoxin B-derived immunomodulatory peptide.

Vibrio cholerae. Escherichia coli.

WO200014114-A1.

16-MAR-2000

99WO-GB02970. 07-SEP-1999;

98GB-0019484 07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor $\mathsf{GM-1}$

Example 5; Page 45; 62pp; English.

The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera coxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CG M-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit ciposyltransferase activity, while the B subunits. The A subunit ciposyltransferase activity, while the B subunits (EtxB and CtxB) and ciposyltransferase activity, while the bost cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible composition such as immunomodulation, are not mediated through GM-1 binding The peptides of the invention (AAY87461-Y87463) are crasments of the beta-4-alpha 2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not cross link GM-1. They may also be used as an inhibitor for immunomodulator or adjuvant. They may also be used as an inhibitor for coxin-induced diarrhoea. Therefore, the peptides may be used in the coxin-induced diarrhoea. Therefore, the peptides may be used in an exemplification of the present invention to assess whether a peptide corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB and CtxB and CtxB and CtxB are immunomodulatory effects. Peptide AAY87465 is a corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB and CtxB as immunomodulatory effects. Peptide AAY87465 is a corresponds to residues.

AA; Sequence

Gaps ó Length 8; Indels 100.0%; Score 39; DB 21; 100.0%; Pred. No. 3.4e+05; tive 0; Mismatches 0; Conservative Query Match Best Local Similarity

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7 EVPGSQH 7 1 evpgsqh g à

AAY87461 RESULT

AAY87461 standard; peptide; 12 AA

AAY87461;

03-JUL-2000 (first entry)

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:3.

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Escherichia coli. Vibrio cholerae.

WO200014114-A1.

16-MAR-2000

99WO-GB02970. 07-SEP-1999; 98GB-0019484. 07-SEP-1998;

(UYBR-) UNIV BRISTOL

Williams NA,

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor $\mathsf{GM-1}$

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                                           The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubjusticous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB).

Thosyltransferase activity, while the B subunits (EtxB and CtxB) accilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain through GM-1 binding is responsible.

Cfor some of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the cornwal EtxB and CtxB subunits, except that they do not bind or cross link GM-1 informy be used in medicine as an immunomodulator or adjuvant.

They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition contain and isorder and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAX87460 being
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant flagellin gene including sequence - for heterologous epitope, and expressed fusion proteins, useful in vaccines and for prodn. of antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 21; Length 12; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; fig.4B; 137pp; English.
               Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP93498 standard; protein; 15 AA.
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Best Local Similarity 100...
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N-PSDB; AAN92414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AA;
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subunit. The DNA sequence encoding this ligates to othersynthetic oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immuno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and esp. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodles mainly of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen; intestines; antibodies; secretory; IgA class.
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100.0%; Pred. No. 0.2;
iive 0; Mismatches 0;
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                                                                                                                                                                Query Match
Best Local Similarity 100..
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Matches 7; Conservative
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2 evpgsqh 8

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Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 39; DB 21; Length 21; 100.0%; Pred. No. 0.28; tive 0; Mismatches 0; Indels
                                                                       Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 15; 62pp; English.
                 AAY87462 standard; peptide; 21 AA.
                                                                                                                                                                                                            98GB-0019484
                                                      (first entry)
                                                                                                                                                                                                                                                Hirst TR;
                                                                                                                                                                                                                              (UYBR-) UNIV BRISTOL.
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                 WPI; 2000-256943/22.
                                                                                                                             Vibrio cholerae.
Escherichia coli.
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                                                                                                                                                        WO200014114-A1.
                                                                                                                                                                                           07-SEP-1999;
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                                                      03-JUL-2000
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                                   AAY87462;
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9
          AAY87462
RESULT
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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the ${\tt glycolipid}$ receptor ${\tt GM-1}$ -

Disclosure; Page 15; 62pp; English.

Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Escherichia coli.

WO200014114-A1.

99WO-GB02970. 98GB-0019484

07-SEP-1999; 07-SEP-1998;

16-MAR-2000

Williams NA, Hirst TR; (UYBR-) UNIV BRISTOL.

WPI; 2000-256943/22.

É. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5.

03-JUL-2000 (first entry)

AAY87463;

AAY87463 standard; peptide; 21 AA.

AAY87463

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The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera conflicts) from vibric oncloses which do not bind to the ubdiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, while the B subunits (EtxB and CtxB) ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and ctxB subunits, except that they do not bind or cross link GM-1 They may be used in medicine as an immunomodulator or adjuvant. They may also be used an an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immunomedisorder and/or toxin-induced diarrhoea. Sequences AAR87460-Y87463 represent preferred peptides of the invention, AAR87460 being particularly preferred.
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The invention relates to peptide fragments of the Escherichia coll heat labile enterotoxin (Etx) and its closely related homologue, cholera to town (Ctx) from vibrio cholerae which do not bind to the ubdiguitous of town in Ctx) from vibrio cholerae which do not bind to the ubdiguitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, while the B subunits (EtxB and CtxB) ribosyltransferase activity, while the B subunits (EtxB and CtxB) across-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx. it has been found that certain effects of the toxins, such as immunomodulation, are not mediated for some of the toxins, such as immunomodulation are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB. exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used as an inhibitor for toxin-induced diarrhoea Therefore, the peptides may be used in medicine as an immunomodulator or adjuvant. Therefore, the peptides may be used in the production of a composition of the composition of the invention and some associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460 being represent preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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AAR76748

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Gaps ö

Conservative

evpgsqh 13

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6 evpgsqh 12
                                                       RESULT
AAP30265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is encoded by a fragment of the the plasmid pLPA93
which was used in the production of fimH fusion genes comprising
the cholera toxin B subunit inserted into the fimH gene. This insert
shows the inclusion of the B subunit into the FimH protein at position
224-226. The chimeric genes were then opt. further modified by insertion
of the hepatitis B virus surface antigen pre-$2 region into a different
position of the FimH adhesin of type I fimbriae. Restriction site handles
(BGIII sites) were introduced into the fimH gene, and the foreign
epitopes are then inserted in-frame. In the selected positions the
insertion of the pitopes did not significantly alter the adhesive
function of the FimH protein. The expression of the chimeric proteins
on the surface of fimbriae on bacterial hosts illustrated the possibility
con the surface of fimbriae on bacterial presenters of foreign antigens and
epitopes. These chimeric genes may be used in the production of variant
confluence in the compounds and maintier genes and miscrobial cells to locations comprising selected receptors to which
                                                                                                                                            FimH; type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue; FimA; FimF; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor specific bacterial adhesins - useful for targetting active compounds and microbial cells to locations of receptors
                                                                                                        Residues 50-64 of cholera toxin B subunit and FimH 224-226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sokurenko EV;
                                                                                                                                                                                                                                                                                                                                                                 "Cholera toxin B subunit 50-64"
                                                                                                                                                                                                                                                                                            /note= "Represents FimH residue 224"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Represents FimH residue 226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pallesen L,
                                                                                                                                                                                                                                                                                                                             'note= "Linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                       "Linker peptide"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 58; 152pp; English.
 AA.
AAR76748 standard; Protein; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molin S,
                                                                                                                                                                                                 Chimeric - Vibrio cholerae.
Chimeric - Escherichia coli.
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 /note=
20..22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1995-275442/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the adhesins bind
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N-PSDB; AAQ93061
                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JAN-1995;
                                                                      18-MAR-1996
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                                    AAR76748;
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                                                                                                                                                                                                                                                                                                              Peptide
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The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                   Sequence of amino acids 50-75 of the cholera toxin B1 subunit which carries an Arg at posns. 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                                                                                                                                                                                                                                    Cholera vaccine; therapy; E.coli infection; enterotoxin LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dodin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rivaille P, Siffert O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP50439 standard; protein; 41 AA.
AAP30265 standard; Protein; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CNRS ) CNRS CENT NAT RECH SCI (INSP ) INST PASTEUR.
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                                                                                                       21-APR-1992 (first entry)
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V, Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1983-834645/49.
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AA;
                                                                                                                                                                                                                                                                                           Vibrio cholerae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milhaud G,
                                                                                                                                                                                                                                                                                                                                               EP95426-A.
                                                   AAP30265;
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Gaps

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Query Match 100.0%; Score 39; DB 16; Length 23; Best Local Similarity 100.0%; Pred. No. 0.31; Matches 7; Conservative 0; Mismatches 0; Indels

EVPGSQH 7

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New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
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1, Delmas A;
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                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                      46 AA;
                                                                                                                                                                                                                                                         17 evpgsgh 23
                                                                                                                                                                                                                                     1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-1983;
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                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                           AAP30600;
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                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                               The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by soild phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                                                                       New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
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                                                                                                                                                                                                                                                                                                                                                                                                    h 100.0%; Score 39; DB 6; Length 41; Similarity 100.0%; Pred. No. 0.55; 7; Conservative 0; Mismatches
           Heat-labile enterotoxin; heat-stable toxin; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat-labile enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                          Claim 8; Page 100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP50436 standard; protein; 46 AA.
                                                                                                       84WO-US02030
                                                                                                                             83US-0559469
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                                                                                                                                                     (SCRI-) SCRIPPS CLINIC RES
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                                                                                                                                                                                                WPI; 1985-159230/26.
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                              41 AA;
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||5 evpgsqh 21
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                                                                                                      12-DEC-1984;
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                                                        WO8502611-A
                                                                                                                                                                        Houghten RA;
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                                                                                20-JUN-1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                    The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of amino acids 350-75 of the cholera toxin B1 subunit which carries an Arg at posns. 35, 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholera vaccine; therapy; E.coli infection; enterotoxin LT
                                                                                                                                                                                                                                                     Length 46;
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                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                 Score 39; DB 6;
Pred. No. 0.62;
Mismatches 0
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Claim 8; Page 100; 120pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 11; 13pp; French
                                                                                                                                                                                                                                                 100.0%;
llarity 100.0%;
Conservative 0;
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nethod has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises: holotoxin for modification by analysing the 3-dimensional form of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structure of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect biological properties of the pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin and the perfusiting toxin and the perfusiting toxin and the perfusiting toxin and the perfusiting toxin and the perfusition of the present sequence represents an ADP-ribosylating toxin and the perfusition of the present sequence represents and perfusion of the present sequence.
                                                                                                                                                                                  ADP-ribosylating toxin, PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method for producing modified pertussis holotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cockle SA, Loosmore S,
                                                                                                                                            Escherichia coli verotoxin-1 B-subunit.
                     AAY41816 standard; peptide; 93 AA.
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94US-0251121.
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                                                                                                      08-DEC-1999 (first entry)
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Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-579908/49.
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                                                                                                                                                                                                                                                Escherichia coli.
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31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1994;
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Hazes B,
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                                                               AAY41816;
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    AAY41816
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                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's blological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes with
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Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hazes B, Klein MH, Loosmore S;
                                                         Query Match 100.0%; Score 39; DB 4; Length 47; Best Local Similarity 100.0%; Pred. No. 0.64; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                           ADP-ribosylating toxin (verotoxin-1 B-subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                    AAR72545 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
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Oomen R, Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                 28-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-132623/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pertussis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 AA;
47 AA;
                                                                                                                                                                 1111111
23 evpgsqh 29
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                                                                                                                                          1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria sp.
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  Sequence
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                                                                                                                                                                                                                                                                                                                             AAR72545;
                                                                                                                                                                                                                                                RESULT 13
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NAME OF THE PROPERTY OF THE PR

Armstrong GD;

Klein MH,

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                                 Gaps
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0
 Length 93;
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Query Match 100.0%; Score 39; DB 20; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                       AAW95226 standard; peptide; 93 AA.
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ID AAW9
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RESULT

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Heat labile toxin B subunit SEQ ID NO:26.
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       NOT COULD COURT OF THE COURT OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods of preparing a pertussis holotoxin (PT) having a modified biological activity. One method comprises identifying at least 1 site in a PT that interacts with a molecule that is capable of forming a complex with the holotoxin and which molecule is an effector molecule which is an adenine nucleotide and which site contributes to toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional structure of crystalline PT, determined by X-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell structure of crystalline PT, determined by X-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The three-dimensional structure of phological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure of PT have functional and/or structural resemblance to other bacterial toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the heat-labile toxin of E. Goli (LT) and verotoxin-1 (VT). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
                                                                                                                                      Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore S;
                                                                                           E. coli heat-labile toxin (LT) beta-subunit sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GD, Cockle SA, Hazes B, Klein MH,
Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY68365 standard; Peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 5; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0292968.
93US-0110947.
94US-0251121.
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                                                (first entry)
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYAL-) UNIV ALBERTA.
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                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA;
                                                                                                                                                                                                              heat-labile; LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 evpgsqh 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong GD,
                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1994;
                                                16-MAR-1999
                                                                                                                                                                                                                                                                                                     US5856122-A.
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                                                                                                                                                                                                                                                                                                                                                   05-JAN-1999
AAW95226;
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Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor; islet-activating protein.
Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin which the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAX68340 to AAX68385 represent peptides used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crystalline form of isolated pertussis holotoxin useful in studying proteins which have functional resemblance -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cockle SA, Loosmore S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 5; 42pp; English.
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94US-0251121
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Matches 7; Conservative
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Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-136703/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 AA;
                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 evpgsqh 47
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                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-1993;
31-MAY-1994;
                                                                                                      immunogenic.
                                                                                                                                                                                                                              US6018022-A
                                                                                                                                                                                                                                                                                             25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The inventors claim vaccines against cholera and heat-labile E.coli toxin contg. cholera toxin fragment coupled to carrier. The toxin is esp. the fragments defined in FT, above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin; structural protein; receptor; heterologous gene; leader; promoter.
                                                                                                                                                                        coli toxin - contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant constructs comprising a promoter functional in Bordetella operatively linked to a heterologous gene or a non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella pertussis; whooping cough; recombinant construct;
                                                                                                                                                                                                                                                                                                                                                               6; Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zealey GR;
                                                                                                                                                                                                                                                                                                                                                               DB 6
1.4;
                                                                                                                                                                         Vaccines against cholera and heat-labile E.
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                          cholera toxin fragment coupled to carrier
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 39; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yacoob RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Figure 1; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW04857 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic cholera toxin B subunit.
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                                                                              (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                       Example; Fig 1; 24pp; German.
                84DE-3430894
                                               83IL-0069558
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.vv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loosmore SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-425088/42.
                                                                                                                                          WPI; 1985-069683/12
                                                                                                                                                                                                                                                                                                                   103 AA;
                                                                                                             Arnon R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT38038
                                                                                                                                                                                                                                                                                                                                                                                                                                                         evpgsqh 57
                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVPGSQH 7
                 22-AUG-1984;
                                                 23-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW04857;
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                           Sela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
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AAW0485
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                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection by Bordetella pertussis.
                                                                                                                                                                                                                                                                                               Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying
                                                                                                                                                                                                                       Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 93;
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                                                                                                                                                                                                                       Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 22
Pred. No. 1.3;
; Mismatches
                                                                                                                                                                                                                       Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; cholera; heat-labile E.coli toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of sub-unit B of cholera toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP50340 standard; protein; 103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "claimed"
45..64
/note= "claimed"
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/note= "claimed"
                                                                                                                                                                                                                       Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 5; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative 0;
                                                                                           98US-0082514
                                                                                                                          94US-0292968
                                                                                                                                       93US-0110947
94US-0251121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                       (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                      Cockle SA,
                                                                                                                                                                                                                                                                  WPI; 2001-122260/13
                                                                                                                                                                                                                                      Stein PE;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 AA;
                                                                                                                                                                                                                                                                                                                                                identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio cholera
                               US6168928-B1
                                                                                           21-MAY-1998;
                                                                                                                                      24-AUG-1993;
31-MAY-1994;
                                                                                                                          22-AUG-1994;
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                                                            02-JAN-2001
                                                                                                                                                                                                                    Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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AAP50340 RESULT

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Gaps

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Bordetella leader sequence for secretion of a gene product which may not be of Bordetella origin, can be used for the expression in Dordetella of Enzymes, antigens, immunogens, allergens, enzyment in Dordetella of enzymes, antigens, immunoglobulins or their inhibitors, hormones, lymphokines, immunoglobulins or their fragments, toxins, mammallan proteins, structural proteins or receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, that promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the constructs are selected from the cholera toxin B leader (CTB-1), the pertussis toxin subunit 31 leader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from a convel synthetic cholera toxin B gene (ctb) and the hmwl and hmw2
                                                                                                                                                                                                                                                                                                                                                                                                                                      genes of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 AA;
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Query Match 100.

Best Local Similarity 100.

Matches 7; Conservative 1 EVPGSQH 7 ò ద

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Gaps

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0; Indels

Mismatches

ó 100.0%; 100.0%;

Score 39; DB 17; Length 103; Pred. No. 1.4;

AAR94939 standard; Protein; 103 AA.

Heat labile enterotoxin B subunit (LT-B) E.coli (first entry) 31-0CT-1996 AAR94939;

Toxin; subunit; vaccine; transgenic plant; immunogen; antigen; adjuvant; immunisation.

Escherichia coli.

WO9612801-A1

02-MAY-1996.

95WO-US13376. 24-OCT-1995;

94US-0328716

24-OCT-1994;

(TULA) TULANE EDUCATIONAL FUND. (TEXA) UNIV TEXAS A & M SYSTEM. Mason HS; Clements JD, Hag TA, Arntzen CJ,

N-PSDB; AAT18799, AAT18800 WPI; 1996-230602/23

Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant Disclosure; Page 100-101; 130pp; English.

an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic A transgenic plant comprising or expressing a DNA sequence encoding

Gaps Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterctoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterctoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross reactivity and are sultable for a broad spectrum vaccine to Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid. Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness ö plant. The immunogenic agent preferably comprises the LT-B or (cholera toxin B subunit) or optionally LT-A or CT-A. Length 103; Indels /label- substitution /note= "wild-type His replaced by Asn" Misc-difference 95 /label= substitution /note= "wild-type Thr replaced by Ala" /label= substitution /note= "wild-type Ala replaced by Ser" ö 100.0%; Score 39; DB 17; 100.0%; Pred. No. 1.4; Chimeric - Vibrio cholerae. Chimeric - Enterotoxigenic Escherichia Coli. 0; Mismatches Location/Qualifiers AAW06606 standard; Protein; 103 AA Claim 3; Page -; 32pp; English. 96WO-SE00570. 95SE-0001682 06-AUG-1997 (first entry) Query Match
Best Local Similarity luv...
7; Conservative vomiting; food poisoning. Holmgren J, Lebens MR; WPI; 1996-506108/50. (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R. Misc-difference 94 103 AA; Misc-difference 1 N-PSDB; AAT43576 51 evpgsqh 57 1 EVPGSQH 7 02-MAY-1996; 05-MAY-1995; WO9634893-A1 07-NOV-1996 Sequence AAW06606; AAW06606 SSXSò Op

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AAW06605)
                                                                                                       Sequence
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(MCGH/) N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                         Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to
protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a voccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                       Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid
                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 1..25
Misc-difference 1..25
/label= substitution
/note= "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
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                                                                                                              Score 39; DB 17; Length 103; Pred. No. 1.4;
                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                         Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic Escherichia Coli.
                                                                                                                                   Mismatches
                                                                                                                                                                                                                         AAW06607 standard; Protein; 103 AA.
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                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                  (first entry)
                                                                                                              Query Match 100.

Best Local Similarity 100.

Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                       vomiting; food poisoning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                   Æ;
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                                                                                                                                                                         51 evpgsqh 57
                                                                                  103
                                                                                                                                                     1 EVPGSQH 7
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                                                               AAW06605)
                                                                                  Sequence
                                                                                                                                                                                                                                              AAW06607
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This is the amino acid sequence of the cholera toxin B subunit used in the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as an mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it enables the possibility for commercial mucosal adjuvants for use in humans, since these are more effective and safer than vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholera toxin B subunit; nontoxic subunit; adjuvant; coadministration;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered
immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                            Length 103;
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with an antigen to birds and mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW80808 standard; protein; 103 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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MCGHEE J R.
TAKEDA Y.
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-594478/50
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                                                                                                                                                                                                                                                                                          103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 evpgsqh 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-1998;
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B subunit of the heat-labile enterotoxin (LT-B) derived from E. coli
                                                   B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malari; circumsporozoite protein; fusion protein; live recombinant vaccine; Salmonella; epitope.
                                                                                                                                                                                                                                                                                                                   Live recombinant vaccine for malaria -
comprising attenuated entero-invasive bacterium contg. DNA
                                                                                                                        /note="Signal peptide"
23..124
                                                                                                                                                                                                                                                                                                                                     encoding epitope of malaria parasite
                                                                                                              Location/Qualifiers
                                                                                                                                                   /note="Mature LT-B"
                                                                                                                                                                                                                                                                   Majarian WR, Pillai S,
                                                                                                                                                                                                                                                                                                                                                       Fig 3; p. 3/17; 105pp; English.
                                                                                                                                                                                                            88WO-US03376.
                                                                                                                                                                                                                                87US-0104735.
                                                                                                                                                                                                                                                 (PRAX-) PRAXIS BIOLOGICS IN.
                  06-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                      WPI; 1989-114399/15.
N-PSDB; AAN90747.
                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evpgsgh 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVPGSQH 7
                                                                                                                                                                                                            30-SEP-1988;
                                                                                                                                                                                                                                02-OCT-1987;
                                                                                                                                                                      W08902924-A
                                                                                                                                                                                          06-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                      multivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
AAP93561;
                                                                                                                                                                                                                                                                     Brey RN,
                                                                                                                       Peptide
                                                                                                                                          Protein
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O.Y
                                     ö
                                                                                                                                                                                                    cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                     Gaps
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New hybrid protein, useful in vaccines -contains cholera toxin b subunit and heterologous IgA active antigenic sequence.
                 100.0%; Score 39; DB 19; Length 103; 100.0%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 39; DB 11; Length 118; ilarity 100.0%; Pred. No. 1.6; Conservative 0; Mismatches 0; Indels (
                                     Indels
                                                                                                                                                                                                                                                                      1..11
/*label= signal peptide
/*note= absent from mature protein
                                    ö
                                    0; Mismatches
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                                                                                                                                                                                                                                             18..18
/*label= His or Tyr
1..11
                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                        AAR04163 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       Martial
                                                                                                                                                                                                                                                                                                                                              89WO-0000495
                                                                                                                                                             (first entry)
                           Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; ; pp; French.
                                                                                                                                                                                 Cholera Toxin B-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                       Renard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
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N-NSDB; Q04046.
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                                                                                                                                                                                                                                                 misc_difference
                                                                  1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                              27-SEP-1989;
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                                                                                                                                                             10-SEP-1990
                                                                                                                                                                                                                                                                                                         WO9003437-A.
                                                                                                                                                                                                                                                                                                                           05-APR-1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                      synthetic
                                                                                                                                         AAR04163;
                   Query Match
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Hockmeyer WT;

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In the patent, the DNA encoding LT-B is expressed as part of a fusion protein with an epitope of a malaria parasite, eg Region I or Region II or a repeat region of circumsporozoite protein antigen (CS) (AAP93560) from Plasmodium berghei. Pref. the fusion gene is inserted into attenuated Salmonelia enteriditis under the left promoter control of amboda. Such bacteria can multiply in the host without causing disease or disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 39; DB 10;
ilarity 100.0%; Pred. No. 1.7;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: July 16, 2001, 16:35:41 Job time: 205 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
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AAP93561 standard; protein; 124 AA.

evpgsqh 68

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RESULT 2 AAP93561

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1 EVPGSQH 7

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Sequence 1, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 6, A Sequence 6, A Sequence 6, A Sequence 4, A Se

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> Sequence 2, Sequence 2, Sequence 13, Sequence 2, Sequence 7,

us-09-786-648-2.rai

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TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
US-08-714-070A-1

US-08-045-806-2

US-09-366-0816-0818-2

US-09-027-337-2

US-08-540-406-6

US-08-55-055-6

US-08-55-1588-6

PCT-US95-1323-6

PCT-US95-1323-6

US-08-602-359A-34

US-08-602-359A-4

US-08-968-752B-4

US-08-968-752B-2

US-08-968-752B-2

US-08-968-752B-2

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US-08-968-752B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAX-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/08292968
| Patent No. 5856122
| GENERAL INFORMATION:
| APPLICANT: READ, Randy J. |
| APPLICANT: COCKLE, Stephen A. |
| APPLICANT: OCOKLE, Stephen A. |
| APPLICANT: LOOSMORE, Sheena |
| APPLICANT: REIN, Michel H. |
| APPLICANT: HAZES, Bart |
| APPLICANT: HAZES, Bart |
| APPLICANT: HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Suite 701, 330 Univers.
CITY: Toronto
COUNTRY: Canada
ZIP: M5G 1R7
COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 100
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-292-968-26
     sequence 5, Appli
Sequence 6, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5223610
Sequence 9, Appli
Patent No. 5194375
Patent No. 5194375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Patent No. 5194375
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Sequence 4, Appli
Sequence 12, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                               July 16, 2001, 16:32:51 ; Search time 30.3 Seconds (without alignments) 4.654 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21,
Sequence 1, A
Sequence 2, A
Sequence 2, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-952-337-1
US-08-952-337-2
US-08-747-410-2
US-08-829-026A-6
US-08-449-045C-4
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US-08-467-956-26
US-08-08-214-26
US-08-952-337-5
US-08-952-337-6
US-08-952-337-6
US-08-952-337-6
US-08-472-111-2
US-09-314-597-2
US-09-374-597-2
US-09-374-597-2
                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
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US-08-694-078-8
US-09-058-260-8
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                                                                                                                                                                                                                                                                                                                         193259 seqs, 20144635 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                       US-09-786-648-2
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Match Length DB
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                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                                                                          APPLICANT: STEIN, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: CCCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOOSWORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg
TELECOMMUNICATION INPORMATION:
TELEPHONE: (416) 595-1155
TELEPROXE: (416) 595-1163
INFORMATION FOR SECTION INPORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/467,536
FILING DATE: 06-JUN-1995
CLASSIFTCATION: 435
FILING APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            ; Sequence 26, Application US/08467536
; Patent No. 5977304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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STRANDEDNESS: si
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: READ, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Ontario
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41 EVPGSQH 47
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41 EVPGSQH 47
                       1 EVPGSQH 7
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                                                                                                                                    RESULT 3
US-08-467-536-26
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                                                              100.0%; Score 39; DB 2; Length 93; 100.0%; Pred. No. 0.56; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: READ.
APPLICANT: READ.
APPLICANT: READ.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
APPLICANT: LOCSWORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBULNEY
STREET: Suite 701, 330 University Avenue
STATE: Ontario
COUNTRY: Canada
                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416, 595-1163
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08467974
Patent No. 5965385
                                                              Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: READ, 1
                                                                                                                                                                                   1111111
41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                       1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                      RESULT 2
US-08-467-974-26
US-08-292-968-26
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Sequence 5, Application US/08952337

Sequence 5, Application US/08952337

Patent No. 6019973

GENERAL INFORMATION:
APPLICANT: HOLDER MICHAEL R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEN HEAT-LABILE
CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT APPLICATION NUMBER: PCT/SE96/00570

EARLIER FILING DATE: 1996-05-02

EARLIER APPLICATION NUMBER: SE 9501682-0

EARLIER APPLICATION NUMBER: SE 9501682-0

SAPTMARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 39; DB 4; Length 93; 100.0%; Pred. No. 0.56; ive 0; Mismatches 0; Indels
                     APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
WUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                     CITY: Toronto
COUTRY: Toronto
COUTRY: Canada
ZIP: MAGG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,514
FILING DATE:
                                                                                                               E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION UNBER: US 08/292,968
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWRRY, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-810
TELECOMUNICATION INFORMATION:
TELEFAN: (416) 595-1155
TELEFAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  APPLICANT: ARMSTRONG, Glen D. APPLICANT: HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
COCANISM: Vibrio cholerae
US-08-952-337-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                       STREET: 6th Fl
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVPGSOH 7
                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 102
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US-08-952-337-5
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                                                                                                                                                                                                                                            TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBUINEY
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/467,976
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTR: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-UNN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-KAY-1994
PRIOR APPLICATION UNDER: US 08/210,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-082-514-26
; Sequence 26, Application US/09082514
; Patent No. 6168928
; GENERAL INFORMATION:
Application US/08467976
                                                             APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKE, Stephen A.
APPLICANT: LOCSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 EVPGSQH 47
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-467-976-26
Sequence 26,
Patent No. 6(
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Gaps

us-09-786-648-2.rai

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GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Yacoob, Reza K
APPLICANT: Saley, Gavin R
APPLICANT: Zealey, Gavin R
APPLICANT: Expension of Gene Products FROM
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2; Length 103; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/894,526 FILING DATE: 01-DEC-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2;
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                           NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1153
TELERAX: 416-595-1163
TELERAX: 065-2457 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-894-526-2; Sequence 2, Application US/08894526; Patent No. 5942418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
100.0%;
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    LENGTH: 103 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 103 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-472-171-2
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                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
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                                                                                                                                                                                                                                                  LENGTH:
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                                                     Gaps
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APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
NUMBER OF SEQUENCES: 56
                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HOLINGTEN, Jan
APPLICANT: HOLINGTEN, Jan
APPLICANT: HOLINGTEN, JAN
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REPERENCE: 346/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT APPLICATION NUMBER: PCT/SS96/00570
EARLIER APPLICATION NUMBER: PS 9501682-0
EARLIER FILING DATE: 1996-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ FOR WINDOWS VEISION 3.0
SEQ ID NO 6
LENGTH: 102
Score 39; DB 3; Length 102;
Pred. No. 0.62;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; score 39; DB 3; Length 102; 100.0%; Pred. No. 0.62; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, Suite 701
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                             Sequence 6, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08472171
Patent No. 5932714
100.0%; Sc
100.0%; Pr
tive 0;
Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Escherichia coli
US-08-952-337-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                   1111111
50 EVPGSQH 56
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50 EVPGSQH 56
                                                                                         1 EVPGSQH 7
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                                                                                                                                                                                               RESULT 7
US-08-952-337-6
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Gaps
                      APPLICANT: Zealey, Gavin ...
APPLICANT: Zealey, Gavin ...
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
TITLE OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tarig A. Hag
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 MCKinney, Suite 5100
CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/393,334
FILING DATE:
CLASSIFICATION OF THE TREBUSE OF THE TREATMENT OF THE TRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.62;
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/09191852
Patent No. 6194560
                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Ontario
COUNTY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATINE
OPERATING SYSTEM: PC-DOS/MS-DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFRENCE/DOCKET NUMBER: 1036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
    Yacoob, Reza K.
Zealey, Gavin R.
Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 103 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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51 EVPGSQH 57
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US-09-191-852-21
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        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Expression of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/33,334
FILING DATE: 23-FEB-1995
ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09013047 Patent No. 5998168 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09374597
Patent No. 6140082
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Loosmore, Sheena M. APPLICANT: Yacoob, Reza K. APPLICANT: Zealey, Gavin R. APPLICANT: Klein, Michel H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LOOSMOre, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 103 amino acids
amino acid
7; Conservative
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                                                                                                                                                                 51 EVPGSQH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||||||||
51 EVPGSQH 57
                                                                                1 EVPGSQH 7
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Matches
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Gaps

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APPLICATION NUMBER: US/09/191,852

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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLERA TOXIN B SUBUNITS
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
GURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1996-01-05
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO. 2
FROM HEAT-LABILE HIDS
                             Query Match 100.0%; Score 39; DB 5; Length 103; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 39; DB 3; Length 123; 100.0%; Pred. No. 0.75;
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                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08952337
Patent No. 6019973
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; ORGANISM: Eschcerichia coli
US-08-952-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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; ORGANISM: Vibrio cholerae
US-08-952-337-1
                                                                                                                                                                                 51 EVPGSQH 57
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                                                                                                                                 1 EVPGSQH 7
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LENGTH: 123
                                                                                                                                                                                                                                                                                        US-08-952-337-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The Texas A&M University System APPLICANT: 310 Wisenbaker APPLICANT: 310 Wisenbaker APPLICANT: College Station, Texas 77843-3369 TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 4; Length 103; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
FILING DATE:
CLASSTEICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W.
REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36170/3P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      NAME: FOX, DAVId L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: P01590US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
PCT-US95-13376-21
Sequence 21, Application PC/TUS9513376
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO: 21:
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COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 103 amino acids
amino acid
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Best Local Similarity 100.
Matches 7; Conservative
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51 EVPGSQH 57
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Patent No. 5770203
GENERAL INFORMATION:
APPLICANT: Burnette, Neal W.
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: Laty De Havilland Drive
CITY: Thousand Oaks
STAREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 39; DB 2; Length 371; 100.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAIL:
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APTENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C
PTLING DATE: 24-MAY-1995
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,026A
FILLIG DATE: 18-AUG-1997
CLASSIFICATION: 435
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Room 411, Bullding 005, BARC-W
CITY: Beltsville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,222
                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-5676
FORMATION FOR 301-504-5060
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                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 371 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-504-5060
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 7; Conservative
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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55 EVPGSQH 61
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                                                                                                             COUNTRY: US
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US-08-449-045C-4
                                                                        CITY: E
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Sequence 6, Application US/08829026A

SEQUENCE INFORMATION: Application A

TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion P
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                                                                                                                               Sequence 2, Application US/08747410

Sequence 2, Application US/08747410

GENERAL IMPORMATION:

APPLICANT: BACGASARIAN, Michael

APPLICANT: BACGASARIAN, CHIMERIC LTB VACCINES

TITLE OF INVENTION: CHIMERIC LTB VACCINES

CORRESPONDENCE: 12

CORRESPONDENCE: 12

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

STREET: Minneapolis

STATE: Minneapolis

STATE: MA
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Pred. No. 0.76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11526.1-US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,410
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
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TELEX:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-747-410-2
                                                                                                                                                                                                                                                                                                                                                                                 USA
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72 EVPGSQH 78
                                     1111111
71 EVPGSQH 77
                 1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
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                                                                                                                             US-08-747-410-2
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us-09-786-648-2.rai

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Gaps
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                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Karathanasis, Sotirios K.
APPLICANT: Ladias, John A.
APPLICANT: Rottman, Jeffrey N.
APPLICANT: Rottman, Jeffrey N.
APPLICANT: Widom, Russell L.
TITLE OF INVENTION: Control of the Apolipoprotein AI Gene
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STAFFE Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                APPLICANT: Burton, Frank H.; Sutcliffe, Gregor
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
                                                                                                                                                                                                                                                                                           DB 6; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.5%; Score 31; DB 1; Length 414; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,471
FILING DATE: 08-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                    Score 33; DB 6
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/784,472
FILING DATE: 24-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CATTOll, Alice 0.
REGISTATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: CMCC-234A
TELECOMMUNICATION INFORMATION:
                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,852
FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
US-08-255-471-9
; Sequence 9, Application US/08255471
; Patent No. 5721096
                                                                                                                                                                                                                                                                                                      84.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 414 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.5
Best Local Similarity 100.
Matches 6; Conservative
                                                                                          HORMONE PROMOTER NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-255-471-9
                                                                                                                                                                                                                                                                                                                                                                                                                             72 EVPSSQH 78
                                                                                                                                                                                                                                                                                                                                                                                       1 EVPGSQH 7
                            5223610
                                                                                                                                                                                                                   LENGTH: 124
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                                                                                                                                                                                                 SEQ ID NO:3
      5223610-3; Patent No.
                                                                                                                                                                                                                                         5223610-3
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GENERAL INFORMATION:
APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1840 De Havilland Drive
CITY: Thousand oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Pred. No. 11;
0; Mismatches 1; Indels
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Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CLASCOUNTRY: USA
ZUP: 91320-1789
ZUP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEMP PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,605A
TITTING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
US-08-435-605A-12
Sequence 12, Application US/08435605A
; Patent No. 5874287
FILING DATE: 06-JUL-1994

ATTORNEY/AGENT INFORMATION:
NAME: MAZEA, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: 4-194
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH 124 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
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ATORNEY/AGENY INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/POCKET NUMBER: A-19
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 124 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-449-045C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-435-605A-12
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RESULT 20 *

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Sequence 8, Application US/08694078
Patent No. 6218163
GENERAL INFORMATION:
APPLICANT: ALLEN, Larry
APPLICANT: ALKEN, John
APPLICANT: FONSTEIN, Michael
APPLICANT: FONSTEIN, Wichael
APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 8
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McDonnell Boennen Hulbert & Berghoff, Ltd. 300 S. Wacker Drive 7th Floor
                                                                        ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive 32nd Floor
CITY: Chicago
                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 10-J8N-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; L6
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 10-TAN-1997
CLASSIFICATION S736
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-UNN-1996
PRIOR APPLICATION NUMBER: US 60/009,704
FILING DATE: 11-CAN-1996
PRIOR APPLICATION NUMBER: US 60/001,995
FILING DATE: 01-AN-1996
FILING DATE: APPLICATION NUMBER: US 60/001,995
FILING DATE: AND NUMBER: US 60/001,995
FILING DATE: 01-ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REGISTRATION NUMBER: 37,293
REGISTRATION NUMBER: 95,963-E
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.9%; Suc
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 329 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-781-802-8
                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                              ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 PGSQH 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-08-694-078-8
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0
                                                                                                                5194375-6
;Patent No. 5194375
APPLICANT: PARK, LINDA S.;GODMIN, RAYMOND G.
ITLE OF INVENTION: DNA ENCODING INTERLEGKIN-7 RECEPTORS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PARK, LINDA S.;GOODWIN, RAYMOND G.
TITLE OF INVENTION: DNA ENCODING INTERLEUKIN-7 RECEPTORS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 30; DB 6; Length 262; 85.7%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 6; Length 459;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                             MUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:
PULICATION NUMBER: US/07/493,588

FILING DATE: 21-MAY-1990

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 421,201

FILING DATE: 13-007-1989

APPLICATION NUMBER: 366,910

FILING DATE: 15-JUN-1989

SEQ ID NO:6:
LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/493,588
FILING DATE: 21-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,201
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: 366,910
FILING DATE: 15-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-781-802-8
Sequence 8, Application US/08781802
Patent No. 5969121
GENERAL INFORMATION:
APPLICANT: ALLEN, Larry
APPLICANT: AIKENS, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIKENS, John
FONSTEIN, Michael
VONSTEIN, Veronika
DEMIRJIAN, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.7*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHODS OF USE

NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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                                    14 EVPGSQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Patent No. 5194375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:4
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5194375-4
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Gaps

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Query Match 76.9%; Score 30; DB 4; Length 329; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUATA:
APPLICATION NUATA:
APPLICATION NUATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUABER: US 60/019,580
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 10-JAN-1996
PRIOR APPLICATION NUMBER: US 60/001,995
FILING DATE: 07-AUG-1995
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,963-C
FILEDAMUNICATION INFORMATION:
TELEPRAX: 312-913-0001
FILEFRAX: 312-913-0002
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TOPE: amino acid
TOPE: Innear
INFORMATIPE: Protein
US-08-694-078-8
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
```

Search completed: July 16, 2001, 16:36:18 Job time: 207 sec

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Gaps

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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	
OM protein – prc	OM protein - protein search, using sw model	
Run on:	July 16, 2001, 16:33:31 ; Search time 34.9 Seconds (without alignments) 15.279 Million cell updates/sec	
Title:	US-09-786-648-2	
Periect score: Sequence:	1 EVPGSQH 7	•
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

219241

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing first

Database : PIR_68:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

DNA-directed RNA p	probable 4-carboxy	probable 3-oxoadip	chorismate synthas	hypothetical prote	flavocytochrome C	hypothetical prote	. interleukin-7 rece	4-aminobutyrate tr	anti-mullerian hor	DNA-binding regula	hypothetical prote	scarecrow-like pro	hypothetical prote	thiamin repressibl	aryl hydrocarbon r
A72247	T47115	T35015	S17246	T47142	B70321	T44138	A34791	JC4022	JC4335	I38155	T22716	T47874	T05041	S41962	A46266
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336	373	375	376	412	436	440	459	200	573	616	622	623	619	775	802
6.94	76.9	76.9	76.9	76.9	76.9	6.94	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	6.97
30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

1	
cholera enterotoxin, B chain precursor VC1456 [validated] - Vibrio cholerae (strain N;Alternate annes: enterotoxin beta chain C:Speries: Vibrio cholerae	train N
C; Date: 24-Apr-1984 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001 C; Accession: \$14624; \$39238; \$39241; H82196; JC1078; \$17666; PC1010; A05130; A01819;	01819;
R; Dams, E.; de Wolf, M.; Dierlck, W. submitted to the EMBL Data Library, March 1991	odo o
A; Description: Correction of the choise a coard national sequence of the figure of th	2010
A; ACCESSION: S14024 A; ACCESSION: A: Type: DA A: Reaidnes: 1-124 < PAM>	
A;Cross-references: EMBL:X58786; NID:948420; PIDN:CAA41593.1; PID:948422 A:Experimental source: strain 2125	
R. Lebens, M.; Holmgren, J. submitted to the EMBL Data Library, November 1993	
A;Description: Structure and arrangement of the Cholera toxin genes in vibrio Cholera	Cholera
A; Accession: S39238	
A;Molecule type: DNA A:Residues: 1-124 <leb></leb>	
A; Cross-references: EMBL: X76390; NID: 9433856; PIDN: CAA53973.1; PID: 9433857	
A; MOlecule type: DNA	
A; Residues: 1-124 <lew></lew>	
A;Cross-references: EMBL:X76391; NID:443869; PIDN:CAA53976 L; PID:94438661 P: DotAd Discourse of the control o	9
Chardson, D.; Ernolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers	Sellers
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.	
Nature 400, 41/7451, 2000. A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.	rae.
A; Reference number: A82035; MUID:20406833	
A; Status; preliminary	
A; Molecule type: DNA	
A; Cross_treferences: GB:AE004224; GB:AE003852; NID:q9655952; PIDN:AAF94613.1; GSPDB A; Cross_treferences: GB:AE00424; GB:AE00424; GB:AE004613.1; GSPDB	SPDB:GM
A; Experimental source: serogroup Ol; strain N16961; biotype El Tor	
R;Sni, C.H.; Cao, C.; Znang, J.S.; Ma, Q.J. Chinese Biochem. J. 9. 395-399, 1993	
A;Title: Nucleotide sequence analysis of the gene encoding the classical biotype V.cl.	pe V.cl.
A; Reference number: JC1078	
A; ACCESSION: OCLO'S A; Molecule type: DNA	
A;Residues: 1-20,'Q',22-31,'Q',33-38,'H',40-49,'G',51-67,'T',69-124 <shi> A;Experimental source: classical biotype strain 569B</shi>	
R; Dams, E.; de Wolf, M.; Dierick, W.	
blochim: blopinys. Actd 1990, 133 141, 1331 A;Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic	classic
A) Metalence number: circol, motel.	

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R;Dallas, W.S.; Falkow, S.
Nature 288, 499-501, 1980
A;Title: Anino acid sequence homology between cholera toxin and Escherichia coll hea—
A;Reference number: A01820; MUID:81074965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Readudes: 11-14 <ORL.
A;Readudes: 11-14 <ORL.
J. Bacteriol. 169, 1352-1357, 1987
A;Tttle: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherich—
A;Tttle: Evolutionary origin of pathogenic A;Reference number: A26946; MUID:87137303
A;Accession: B26946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1.-27, FE., 29-63, 'K', 65-124 < YAM>
A; Residues: 1.-27, FE., 29-63, 'K', 65-124 < YAM>
A; Cross references: EMBL: M15363; NID: g148335; PIDN: AA24792.1; PID: g148336
A; Cross references: EMBL: M15363; M.S.
R; Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect. Immun. 48, 73-77, 1985
A; Title: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons=
A; Ritle: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons=
A; Reference number: 141194; MUID: 85156481
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A; Residues: 1-5, F', 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17
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A; Residues: 1-22 <RE2>
A; Residues: 1-22 <RE2>
A; Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
B; Cross-references: GB:M17101, IIImamura, S.; Miyama, A.
B; Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
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A; Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic
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A; Residues: 1-17, 'C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124 —
A; Residues: 1-17,'C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124 —
A; Cross-references: GB: S60731; NID: 9408994; PIDN: AAC60441.1; PID: 9408996
R: Feuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.—
Microb. Pathog. 2, 381-390, 1987
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J. Biol. Chem. 262, 10189-10194, 1987
A;Title: A functional interaction between the signal peptide and the translation app==
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin Reference number: A61475; MUID:89180953
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A;Residues: 22-24,'S',26-27,'E',29-63,'K',65-66,'A',68-95,'A',97-122,'E',124 <TSU>
A:Experimental source: strain 240-3
                                                                                                                                                                             C;Species: Escherichia coli
C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999
C;Accession: A01820; B26946; 141194; 141287; 167644; A61475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the toxin is produced by
                                                                                                                                    heat-labile enterotoxin chain B precursor - Escherichia coli
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A;Accession: 141287
A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No.
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Best Local Similarity
7; Conserve
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A. Ancession: S1757, 1983 A. Ancession: Ance
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Conservative

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Query Match

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DB 1; Length 124; Indels

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hypothetical protein - Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 26-May-2000
C; Accession: B27586
R; Booth, R.J.; Harris, D.P.; Love, J.M.; Watson, J.D.
J. Immunol. 140, 597-601, 1988
A; Title: Antiquaic proteins of Mycobacterium leprae. Complete sequence of the gene fo A; Reference number: A92821; MuID:88088878
A; Accession: B27586
                                                                                                                                                                                                                                                                                                                                         A;Residues: 1455 <KKNN>
A;Cross-references: GB:299105; GB:AL009126; NID:92632457; PIDN:CAB12043.1; PID:926325
A;Experimental source: strain 168
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C.Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C.Accession: S44886
B.Du. Z.
submitted to the EMBL Data Library, May 1993
A.Bescription: Sequence of the C. elegans cosmid ZK112.
A.Reference number: S44616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:L14324; NID:g289740; PID:g289741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 25/3; 65/2; 196/2; 249/1; 275/1; 385/2; 415/2
C;Superfamily: Caenorhabditis elegans ZK688.6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 1
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: ycbF
C;Superfamily: glucarate dehydratase
C;Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2K112.1 protein - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.1%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
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Best Local Similarity 71.*
5. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-534 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 EIPGSAH 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||| :|
64 EVPGGEH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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S44886
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Withdraugh 20-oxidase - common tobacco)
Cipter at a manes: Nto16 protein
Cipter 3 Micotiana tabacum (common tobacco)
Cipter 19-reb-1999 #sequence_revision 19-reb-1999 #text_change 20-Jun-2000
Citer 19-reb-1999 #sequence_revision 19-reb-1999 #text_change 20-Jun-2000
Citer 20-1999 #sequence_revision 19-reb-1999 #text_change 20-Jun-2000
Citer 20-20-1999 #sequence_revision 19-reb-1999 #text_change 20-Jun-2000
Citer 20-20-1999 #sequence_revision 19-reb-1999 #text_change 20-Jun-2000
Ry Tanaka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M.;
Ry Tanaka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M.;
Reference number: 214418
A; Reference number: 214418
A; Accession: T01751
A; Accession: T01751
A; Molecule type: mRNA
A; Residues: 1-367 cTAN>
A; Coss-references: EMBL: Ab016084
C; Genetics:
A; Coss-references: EMBL: Ab016084
C; Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucarate dehydratase (EC 4.2.1.40) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A69753
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex
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                                                                                                                                                                    C: Species: Hono sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14755
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenbuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z18181
A;Accession: T14755
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-272 <WAM>
A;Cross references: EMBL:AL110209
A;Experimental source: fetal brain; clone DKFZp564A0122
C:Genetics:
A;Note: DKFZp564A0122.1
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Pred. No. 17;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 2
Pred. No. 23;
0; Mismatches
                                                                                                                                                     protein DKFZp564A0122.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 84.6
Best Local Similarity 71.4
Matches 5; Conservative
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246 ELPGSEH 252
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149 EVPSSQH 155
         IIIIIII
EVPGSQH 78
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                                                                                                                                                     hypothetical
                                72
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C; Species: Halobacterium Sp. NRC-1
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: G84353
R; My, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
Jung, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitzs, T.
Froitzs, T. 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A; Reference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Species: Deinococcus radiodurans
C. Date: 03-Dec-11999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C. Accession: H75446
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
                                                                                                                                                                                                                                                                                                                                                               R;Beauchemin, M.; Savard, P.
Dov. Biol. 154, 55-65, 1992
A;Title: Two distal-less related homeobox-containing genes expressed in regeneration
A;Fitle: Two distal-less related homeobox-containing genes expressed in regeneration
A;Reference number: A48820; MUID:93050784
A;Accession: B48820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross_references: GB:X63531; GB:S47223; NID:g432377; PIDN:CAA45094.1; PID:g432378
A;Note: sequence extracted from NCBI backbone (NCBIN:117052, NCBIP:117053)
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Steywords: DNA binding; homeobox; nucleus; transcription regulation
F;126-182/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                  homeobox protein (clone NvHBox-4) - eastern newt
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H75446
(S)-2-hydroxy-acid oxidase - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 274;
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46;
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Pred. No. 45;
1; Mismatches
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Pred. No. 4
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71.4%;
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71.48;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-273 <BEA>
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A:Molecule type: DNA
A:Residues: 1-274 <STO>
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Best Local Similarity
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117 EAPGDQH 123
                                           :111 11
66 KVPGKQH 72
                                                                                                                                                                                                                                                                                                                                 C; Accession: B48820
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          EVPGSQH
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96B27
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Status: prellminary
A;Molecule type: DNA
A;Residues: Liefo (STD)
A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C; Cate: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C; Accession: 734767
R; Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, August 1998
A; Reference number: 221556
A; Accession: 734767
A; Accession: 734767
A; Accession: 734767
A; Catesion: 1-342 August
A; Molecule type: DNA
A; Redidues: 1-342 August
A; Rolecule type: DNA
A; Residues: 1-342 August
A; Cross-references: EMBL:AL031184; PIDN:CAA20190.1; GSPDB:GN00070; SCOEDB:SC2A11.21c
A; Experimental source: strain A3(2)
C; Genetics:
A; Genetics:
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C;Genetics:
A;Residues: 1-137 <BOO>
A;Cross-references: GB:M19058; NID:g149919; PIDN:AAA88230.1; PID:g1196505
C;Superfamily: Mycobacterium leprae hypothetical 15.2K protein
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                     Length 137;
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                                                                                                                                                                  Score 31; DB 2
Pred. No. 22;
1; Mismatches
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Pred. No. 40;
1; Mismatches
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Pred. No. 43;
1; Mismatches
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71.4%;
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71.48;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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5; Conservative
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205 EVPGTDH 211
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Best Local S
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Matches 1

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apolipoprotein A-I regulatory protein 1 - mouse
NyAlternate names: ARP-1 protein; COUP-TFII
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Sep-1999
C; Accession: I48975; I48732; S44284
R; Qiu, Y; Cooney, A.J; Kurstani, S; DeMayo, F.J.; Tsai, S.Y.; Tsai, M.J.
Proc. Natl. Acad. Sci. U.S.A. 91, 4451-4455, 1994
A;Title: Spatiotemporal expression patterns of chicken ovalbumin upstream promoter-tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U07635; NID:9466469; PIDN:AAA19854.1; PID:9466470
R;Jonk, L,J.; de Jonge, M.E.; Pals, C.E.; Wissink, S.; Vervaart, J.M.; Schoorlemmer, Mech. Dov. 47, 81-97, 1994
Mech. Dov. 47, 81-97, 1994
A;Title: Cloning and expression during development of three murine members of the COU A;Reference number: 148305; MUID:95034311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16 T46725 chorismate synthase (EC 4.6.1.4) / flavin reductase, NADPH-dependent [validated] - Ne
                                                                                                                                                                                                                                                                                                                                                                                                                              protein homology
factor; zinc finge
Gene Expr. 1, 207-216, 1991
A;Title: The COUP-TFS compose a family of functionally related transcription factors.
A;Reference number: I54072; MUID:92314709
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A;Residues: 1-35,'P',37-414 <RE2>
A;Cross-references: EMBL:X76653; NID:g482927; PIDN:CAA54096.1; PID:g482928
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A,Map position: 15526.1-15526.2
C;Superfamily: unassigned erbA-related proteins; erbA transforming C;Keywords: DNA binding; lipid binding; lipoprotein; transcription F;77-323/Domain: erbA transforming protein homology <ERBA>
F;79-99/Region: zinc finger
F;115-139/Region: zinc finger
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A;Molecule type: mRNA
A;Residues: 1-414 <RES>
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100.0%; Pred. No. 71;
iive 0; Mismatches
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Pred. No.
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A; Accession: 148975
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-351 <RES>
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A; Status: translated from GB/EMBL/DDBJ
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100.0%; Pr
tive 0;
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Matches 6; Conserv
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Matches 6; Conserv
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|4 EVPGSQ 19
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                                                                                                     A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Rieslance number: A75250; MUID:20036896
A.Roceslanc: H75446
A.Roceslanc: H75446
A.Rocelle type: DNA
A.Roceslance: 1-353 < WHID:
A.Rocelle type: DNA
A.Roceslance: 1-353 < WHID:
A.Rocelle type: DNA
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A;Reference number: A81500; MUID:20150255
A;Reference number: D81715
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <TET>
A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719037
A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C;Date: 31.Mar-2000 #sequence_revision 31.Mar-2000 #text_change 11-May-2000
C;Accession: D81715
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
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       , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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A,Map position: 1
C,Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
F;3-297/Domain: (S)-2-hydroxy-acid oxidase homology
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A,Residues: 1-414 <LAD>
A;Cross-references: GB:M64497; NID:g179023; PIDN:AAA86429.1; PID:g179024
R;Wang, L.H.; Ing, N.H.; Tsal, S.Y.; O'Malley, B.W.; Tsal, M.J.
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Science 251, 561-565, 1991
A.Title: Regulation of the apolipoprotein AI gene by ARP-1, a novel
A;Reference number: A37133; MUID:91118002
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63;
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60;
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Pred. No. (
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Pred. No.
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83.3%;
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Best Local Similarity 83.3
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Best Local Similarity
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327 LPGSQH 332
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A;Title: Organization of the murine and human interleukin-7 receptor genes: two mRNAs A;Reference number: A40256; MUID:91246172
A;Accession: C40256
                  Cell 60, 941-951, 1990
A;Title: Cloning of the human and murine interleukin-7 receptors: demonstration of a A; Reference number: A34791; MUID:90199875
A;Accession: D34791
A;Molecule type: mRNA
A;Residues: 1-459 <GGO>
A;Cross-references: GENZ99697; NID:9198377; PIDN:AAA39304.1; PID:9309411
R;Pleinan, C.M.; Gimpel, S.D.; Park, L.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F. Mol. Cell. Biol. 11, 3052-3059, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O.; Alon
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A;Cross-references: EMBL:282062; PIDN:CAB04890.1; GSPDB:GN00019; CESP:W02A11.3
A;Experimental source: clone W02A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 231-239; 264-272 <PLE>
A; Residues: 231-239; 264-272 <PLE>
C; Superfamily: interleukin-7 receptor; fibronectin type III repeat homology
C; Keywords: cytckine receptor; phosphoprotein; transmembrane protein
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-459/Product: interleukin-7 receptor #status predicted <MAT>
F; 21-239/Domain: extracellular #status predicted <EXT>
F; 240-264/Domain: transmembrane #status predicted <TWM>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T26069
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A;Molecule type: DNA
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A; Reference number: 220147
A; Accession: T26069
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Pred. No. 85;
1; Mismatches
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C;Superfamily: RING finger homology
F;429-479/Domain: RING finger homology <RRN>
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Pred. No.
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85.7%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 85...
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N;Contains: chorismate synthase (EC 4.6.1.4); flavin reductase, NADPH-dependent C;Species: Neurospora crassa C;Date: 17-Mar-2000 #text_Change 02-Sep-2000 C;Accession: T46725 R;Henstrand, J.M.; Amrhein, N.; Schmid, J. J. Balol. Chem. 270, 20447-20452, 1995 A;Ttle: Cloning and Characterization of a Heterologously Expressed Bifunctional Chorism A;Reference number: 206450; MUID:95386486 A;Accession: T46725 
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 23-Jul-1999
C;Accession: D34791; C40256
R;Goodwin, R.G.; Friend, D.; Ziegler, S.F.; Jerzy, R.; Falk, B.A.; Gimpel, S.; Cosman,
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Pred. No. 74;
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Matches 6; Conservative
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274 EVPGSIH 280

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Query Match

Query Match Best Local Similarity Matches 6; Conserv

11111 | 274 EVPGSIH 280

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C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology F;237-294/Domain: immunoglobulin homology <IMM>
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: A43425
R; Kayyem, J.F.; Roman, J.M.; de la Rosa, E.J.; Schwarz, U.; Dreyer, W.J.
J. Cell Biol. 118, 1259-1270, 1992
J. Cell Biol. 118, 1259-1270, 1992
J. Ritte: Bravo/Nr-CAM is closely related to the cell adhesion molecules L1 and Ng-CAM is A; Reference number: A43425; MUID:92381110
A; Reference number: A43425
A; Status: preliminary; not compared with conceptual translation
A; Rolecule type: nucleic acid; protein
A; Rosidues: 1-1259 KAAz>
A; Residues: 1-1259 KAAz>
A; Reperimental source: cerebellum
A; Rosidues was acceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Algorithms of the EMBL Data Library, March 1995
Albescription: The sequence of C. elegans cosmid B0228.
Albescription: The sequence of C. elegans cosmid B0228.
Albescription: T29041
Albert T29041
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C; Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 04-Mar-2000
C;Accession: T29041
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C;Date: 27-Apr:1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
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Bravo/Nr-CAM cell adhesion molecule L1 homolog - chicken (fragment)
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Pred. No. 1.9e+02;
1; Mismatches 0; Indels
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Pred. No. 2.3e+02;
0; Mismatches 1; Indels
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85.7%;
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illarity 83.3%;
Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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A; Residues: 1-1028 <STO>
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Best Local Similarity
Matches 5; Conserv
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A, Map position: 1
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C; Accession: T2
R; Leimbach, D.
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: B72782
B;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
A;Accession: B72782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-148 <KAW>
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79156.1; PID:d1042932; PID:g
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A; Cross-references: EMBL: AF016416; PIDN: AAB65273.1; GSPDB:GN00020; CESP:F29A7.3
A; Experimental source: strain Bristol N2; clone F29A7
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C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Accession: T31701
A; Description: The sequence of C. elegans cosmid F29A7.
A; Reference number: 221071
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
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  Length 1259,
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                                               0; Indels
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C;Superfamily: Aeropyrum pernix hypothetical protein APE0243
                                                                                                                                                                                                                                                         hypothetical protein APE0243 - Aeropyrum pernix (strain K1)
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hypothetical protein F29A7.3 - Caenorhabditis elegans
79.5%; Score 31; DB 2; L 100.0%; Pred. No. 2.3e+02; iive 0; Mismatches 0;
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Pred. No. 39;
0; Mismatches
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Pred. No. 40;
0; Mismatches
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100.0%; Pre
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                                                 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
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Best Local Similarity
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A; Molecule type: DNA
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| EVPGSQ 656
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Conserved hypothetical protein PA0054 [imported] - Pseudomonas aeruginosa (strain PA01) Conserved hypothetical protein PA0054 [imported] - Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Dseudomonas aeruginosa C; Species: Dseudomonas aeruginosa S; September: Dseudomonas aeruginosa S; Van, Y; Pham, X; Pand, Y; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A; Reference number: A82950; MUD: 20437337
A; Reference number: A82950; MUD: 20437337
A; Molecule type: DNA
A; Residues: 1-182 cSTO-A; CSTO-A; CSSS-references: GB: AE004445; GB: AE004091; NID: 99945872; PIDN: AAG03444.1; GSPDB: GN001
C; Genetics: A; Genetics: A80054
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Pred. No. 48;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Search completed: July 16, 2001, 16:37:00 Job time: 209 sec

2 VPGSQH 7 ||||:| |118 VPGSRH 123

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July 16, 2001, 16:35:46; search time 57.41 Seconds (without alignments) 16.132 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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39
1 EVPGSQH 7
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Perfect score:
Sequence:
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sp_unclassified:*
sp_vertebrate:*
sp_virus:* sp_invertebrate:* sp_mammal:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	01000	Query	1000	9	ď.	
	2000	Marci	accii beligirii bb	a :		Description
7	39	100.0	103	~	Q9R646	O9r646 vibrio chol
7	39	100.0	124	7	057193	vibrio
რ	39	100.0	124	7	Q56635	
4	39	100.0	124	~	Q9RP15	vibrio
ស	35	89.7	565	10	022511	022511 vitis vinif
9	34	87.2	195	13	Q9W7D3	09w7d3 orvzias lat
7	34	87.2	199	13	Q9W7D4	09w7d4 orvzias lat
ω	34	87.2	201	7	Q9RJZ8	O9riz8 streptomyce
σ	33	84.6	192	4	90an60	
10	33	84.6	272	4	Q9UG04	Q9uq04 homo sapien
11	33	84.6	367	10	080418	
12	33	84.6	412	4	Q9Y2B3	Q9y2b3 homo sapien
13	33	84.6	898	2	Q9VFE2	Q9vfe2 drosophila
14	32	82.1	95	10	Q9FQ18	Q9fqi8 amaranthus
15	32	82.1	765	11	070284	O70284 mus musculu
16	31	79.5	95	10	Q9FQJ8	Q9fq18 amaranthus
17	31	79.5	122	N	Q9W2V0	Q9w2v0 drosophila
18	31	79.5		11	Q9JL95	091195 mus musculu
19	31	79.5		7	086582	086582 streptomyce
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Gaps ô

Query Match 100.0%; Score 39; DB 2; Length 103; Best Local Similarity 100.0%; Pred. No. 0.71; Matches 7; Conservative 0; Mismatches 0; Indels

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RESULT Q57193 ID Q57: AC Q57: DT 01-1 DT 01-1 DT 01-1 DT 01-1 DE CHO:

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		SULT 1 2646 Q9R646 Q9R646 Q9R646 01-MAY-200 01-MAY-200 01-CT-200 CHOLTEAN CHOLTEAN NCBL_TAXII [1] 1] NCBL_TAXII 1] NCBL_TAXII 1] NCBL_TAXII 1] NCBL_TAXII 1] NCBL_TAXII 1] NCBL_TAXII 1] NCBL_TAXII 1] NCBL_TAXII NCBL_TAXIII 1] NCBL_TAXIII 1] NCBL_TAXIII 1] NCBL_TAXIII NCBL_T

9057193 PRELIMINARY; PRT: 124 AA.
057193;
01-NOV-1996 (TERMELREL: 01, Created)
01-NOV-1996 (TERMELREL: 01, Last sequence update)
01-OCT-2000 (TERMELREL: 15, Last annotation update)
CHOLERA TOXIN B PROJEIN (CTB) PRECURSOR (CTB).

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Gaps

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Eukaryota; Viridiplaníae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.
NCBL_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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SEQUENCE FROM N.A.
TATALIA-CV. THOMBOON SEEDLESS (CLONE 2A); TISSUE-FRUIT;...
Cassol T., Adams D.O.
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES CLASS.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=KNIH002;
STRAIN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C.,
Cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misainmurhag Hoiji 35.205-210(1999).
EMBL; AF175708; AAD51360.1; -...
HSSP: P01556; 2CHB.
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                                                                                                                           0; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAR-2091 (TrEMBLrel. 16, Last annotation update)
GLUTARHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERS ENTEROTOXIN B-SUBBNIT.
                                                                        DB 2;
0.86;
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                                                                        Score 39;
Pred. No.
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Mendel, 26381, Vitvi,1190,26381.
InterPro, IPR000103; -
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100.0%;
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                                                Query Match
Best Local Similarity 100...
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Best Local Similarity 100.

Matches 7; Conservative
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  SEQUENCE
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                                                                                                                      "Comparison of cholera toxin genes (ctxAB) of non-Ol vibrio cholerae strains 854 (0139-bengal) and 87 (037) from two outbreaks."; Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases. EMBL; D30052; BAA06289.1; -. HSSP; P01556; 2CHB.
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                          Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxiD=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHOLERA TOXIN B PROTEIN (CTB). D6BF83FFF7924EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 39; DB 2; Length 124; 100.0%; Pred. No. 0.86;
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X58785; CAA41591.1; -.
EMBL; W256795 AAC34728.1; -.
EMBL; A00931; CAA00098.1; -.
HSSP; P01556; 2CHB.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 STRAIN-CLASSICAL BIOTYPE 569B;
Shi C., Cao C., Zhang J., Ma Q.;
Chin. Biochem. J. 9:395-399(1993).
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Pfam; PF001376; EnterOtoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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22 124 C
124 AA; 13919 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CLASSICAL BIOTYPE 569B;
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Best Local Similarity 100.

Matches 7; Conservative
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72 EVPGSQH 78
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SIGNAL
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Kanamori A.; ^{\circ}Systematic identification of genes expressed during early obgenesis
                                                                                                                                                                                                                                                87.2%; Score 34; DB 13; Length 199;
100.0%; Pred. No. 16;
iive 0; Mismatches 0; Indels
                                                      in medaka.";
Mol. Reprod. Dev. 0:0-0/1999).
EMBL: AF128817. AAD38914.1; -.
Hypothetical protein.
SEQUENCE 199 AA: 21726 MW; E9827C05451B15CD CRC64;
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 13, Last annotation update)
01-NOV-1999 (TrEMBLrel. 13, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last an
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                                                                                                                                                                                                                                                                                                                                89.7%; Score 35; DB 10; Length 565; 71.4%; Pred. No. 28;
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                      Primer, provided: 1. Presservity of Primer provided: Pro
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EMBL. AF128818; AAD38915.1; -.
Hypothetical protein.
SEQUENCE 195 AA; 21446 MW; B90682D695729E88 CRC64;
                                                                                                                                                                                                                                                565 AA; 60695 MW; B26113AE09A121DE CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHERICAL 21.7 KDA PROTEIN.
Oryzias latipes (Medaka fish).
                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 AA
                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.2
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                   Query Match 89.7
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
InterPro; IPR001100; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=ORANGE-RED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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239 EIPGSEH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in medaka.";
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                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9W7D3
Q9W7D3;
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Q9W7D4;
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Q9W7D3
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Q9W7D4
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Rinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL13210; CAB61584.1;
InterPro; IPPR002502:--.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                          Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
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Pred. No. 16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cerdeno A. M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   Oliver K., Harris D.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01510; Amidase_2; 1.
SEQUENCE 201 AA; 22749 MW; BBEF477E06A20468 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
11DPL, LCAT-LIKE LYSOPHOSPHOLIPASE (FRAGMENT).
                                                                                       Last sequence update)
Last annotation update)
201 AA
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                                                         Created)
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   PRT;
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Gaps

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1; Indels

Length 367;

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                                                                                                       Tanaka-Ueguchi M., Itoh H., Oyama N., Koshioka M., Matsuoka M., "Over-expression of a tobacco homeobox gene, NTH15, decreases the expression of a gibberellin biosynthetic gene encoding GA 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and expression of a novel lysophospholipase which structurally resembles lecithin cholesterol acyltransferase."; Biochem. Biophys. Res. Commun. 257:50-56(1999).
EMBL; 4017494; BAR76877.1; -...
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01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAR-2000 (TIEMBLrel. 13, Last sequence update)
01-MAR-2001 (TIEMBLrel. 16, Last annotation update)
CG3837 PROTEIN.
CG3837.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99194552; PubMed-10092508;
Tanlyama Y., Shibata S., Kita S., Horikoshi K., Shirafuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.6%; Score 33; DB 4; Length 412;
ilarity 71.4%; Pred. No. 53;
Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                       Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABOLGO84; BAA31690.1; -.
Mendel; JUG81; Nicta;2972;31081.
InterPro; IPR002419; -.
                                                                                                                                                                                                                                                                                                  Pfam; PF00671; Fe_Asc_oxidored; 1.
SEQUENCE 367 AA; 42170 MW; 923BC90B3BBBAC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF02450; LACT; 1.
SEQUENCE 412 AA; 46657 MW; 1FBA8A5783AF050A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 10;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      868 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                 84.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCAT-LIKE PROTEIN (LLPL).
                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sumino Y., Fujino M.;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 EVPSSQH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|||:|
386 ELPGSEH 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVPGSQH 7
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                                                                                                                                                                                                      oxidase.
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                                                                                                                                                                                                                     Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for integrated Molecular analysis of
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI10209; CAB53675.1; -.
InterPro: IPR003386; -.
Pfam: PF02450; LACT; 1.
Hypothetical protein.
SEQUENCE 272 AA; 31016 MW; ACCC5E1680D7A720 CRC64;
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0
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Pred. No. 24;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 4; Length 272;
Pred. No. 35;
2; Mismatches 0; Indels
                                                                                                                       SEQUENCE FROM N.A. Pluvinet R., Sumoy L.; Sluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389957;
OND TER
SEQUENCE 192 AA; 21609 MW; 04A7AE8CB344F213 CRC64;
                                                                                                                                                                                                                                                                                                                                                             192 AA; 21609 MW; 04A7AE8CB344F213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETCAL 31.0 KDA PROTEIN.
DKF2P564A0122.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 AA.
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080418,
01-NOV-1898 (TEMBLEEL: 08, L,
01-NOV-1998 (TEMBLEEL: 08, L,
01-JUN-2000 (TEMBLEEL: 14, L,
NTC16 PROTEIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                   84.6%;
71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 84.6
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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166 ELPGSEH 172
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246 ELPGSEH 252
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RESULT 11 080418 ID 080418 AC 080418 DT 01-NOV DT 01-NOV DT 01-JUN DT 01-JUN DT 01-JUN ON NTC16 GN NTC16

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RA Adams M.D., Celniker S.E., 119 P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., 119 P.W., Hoskins R.A., Galle R.F.,
Ramaratides P.G., Scherer S.E., 119 P.W., Hoskins R.A., Galle R.F.,
Ramaratides P.G., Scherer S.E., 119 P.W., Hoskins R.A., Galle R.E.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Ramando R.C., Rogers Y.H.C., Bazel R.G., Champe M., Petalffer B.D.,
Ram Abril J.F., Agbayani A., An H.-J., Andrews Pfenanch.C., Baldwin D.,
Ballew R.M., Basu A., Baxendalle J., Bayraktaroglu L., Beasley E.M.,
Ram Bescon K.Y., Dence P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ram Borkova D., Botchan M.R., Bouk J., Bayraktaroglu L., Beasley E.M.,
Ram Borkova D., Botchan M.R., Bouk J., Brokstein P., Brottler P., Sorther A., Chandra I.,
Ram Cherry J.M., Cawley S., Dahler H., Cadleu E., Center A., Chandra I.,
Ram Cherry J.M., Cawley S., Dahler H., Cadleu E., Chard P. B.,
Ram Cherry J.M., Cawley S., Dahler H., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Ram Cherry J.M., Cawley S., Correll J.H., Gu Z., Gann P., Harris M.,
Rautis N.L., Harvey D., Henman T.J., Hernandez J.R., Houck J.,
Ram Harris N.L., Harvey D., Henman T.J., Hernandez J.R., Houck J.,
Ram Harris N.L., Harvey D., Helman T.C., Melmel D., Lai Z.,
Ram Harris N.L., Marrey D., McLod M.P., McDay M. C.,
Alalali M., Kalush F., Karaft C., Kravitz S., Kalp D., Lai Z.,
Ram Kimmel B.Z., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,
Ram Kimmel B.Z., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,
Ram Kimmel B.Z., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,
Ram Kimmel B.N., Nelson K.A., Nivon K., Nivos K., Muzny D.M., Naron K.,
Ram Kimmel B.N., Nelson K.A., Nivon K., Nivos K., March S., Roll E.,
Ram Shirskas R., Tecfor C., Turner R., Vertic B., Wang A.,
Ram Saarman D.A., Weilner E., Wang A., Wang Z.,
Ram Shirskas R., Tecfor C., Turner R., Wenter E., Wang A., Wang Z.,
Ram Shirskas R., Redoctor C., Turner R., Weill Seenlow S., Wang A.,
Ram Shirskas R., Redoctor C., Turner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLE-1. 16, Last annotation update)
Amaranthus guitensis.
Amaranthus quitensis.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 84.6%; Score 33; DB 5; Length 868; Best Local Similarity 71.4%; Pred. No. 1.1e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  868 AA; 98349 MW; F6562A64E72E7B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001777; .. Pfam; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||:||
812 ELPGTOH 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVPGSOH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FQI8;
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Q9FQI8
      OS ED DE DE SO
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97020303; PubMed-8812055; MEDLINE-97020303; PubMed-8812055; Kuwana E., Bulfone A., Fletcher C.F., Copeland N.G., Jenkins N.A., Crews S., Martinez S., Puelles L., Rubenstein J.L., Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                 ó
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Amaranthaceae; Amaranthus.
NCBL_TaxID=107609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Expression patterns of two murine homologs of Drosophila minded suggest possible roles in embryonic patterning and pathogenesis of Down syndrome.";
                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 10; Length 95;
Pred. No. 20;
1; Mismatches 1; Indels
                                                                                                                                                                                retrotransposons in plants.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF232993; AAG44333.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    May N.R., Fan C.-M.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF038857; AAC05481.1; -
EMBL: AF044913; AAC05481.1; JOINED.
                                                                                                                                   He Y., Sun M.; "Reverse transcriptase sequence evolution in copia-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAC; 1.
AA; 85575 MW; 46AC6BFD8A189126 CRC64;
                                                                                                                                                                                                                                                                                                 95 AA; 11392 MW; 8E931447E1683C5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 11;
Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          765 AA
                                                                                                             TRANSPOSON-COPIA-LIKE RETROTRANSPOSON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF038853; AAC05481.1; JOINED.
EMBL; AF038854; AAC05481.1; JOINED.
EMBL; AF038855; AAC05481.1; JOINED.
EMBL; AF038856; AAC05481.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                    82.1%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01, MAR-2001 (TrEMBLrel. 16, SINGLE-MINDED PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001610; -
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Pfam; PF00989; PAS; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003015;
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Best Local Similarity
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SEQUENCE 765 A
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26 EVPGKEH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVPGSQH 7
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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Gaps
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                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Amaranthaceae; Amaranthus.
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                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 10; Length 95;
Pred. No. 32;
2; Mismatches 1; Indels
 Indels
                                                                                                                                                                                                                                                                    He Y., Sun M.;
"Reverse transcriptase sequence evolution in copia-like retrotransposons in plants.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF232981; AAG44323.1; -.
                                                                                                                                                                                                                                                                                                                                                        95 AA; 11241 MW; 36403CBDC40D769A CRC64;
                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
REVERSE TRANSCRIPTAGE-LIKE PROTEIN (FRAGMENT)
Amaranthus quitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
 1;
                                                                                                        95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AA
 Mismatches
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TRANSPOSON=COPIA-LIKE RETROTRANSPOSON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                        PRT;
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MEDLINE-20196006; Pubmed-10731132;
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                                                                                                                                                                                                                                                                                                                                                                                            79.5%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, CG15303 PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 79.5
Best Local Similarity 57.1
Matches 4; Conservative
6; Conservative
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=107609;
                                      423 ERPGSQH 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|| :|
26 EIPGKEH 32
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                     1 EVPGSQH 7
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NON_TER
SEQUENCE
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                                                                                RESULT 16
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Matches
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Foblar C., Gabrielland A.E., Garg N.S., Gelbart W M.A., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Gluan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hortin D., Houston K.A., Howland T.J., Wei M.-H., Ibeeyam C., Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Lasko P., Leil Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lu X., Mattei B., MoIntosh T.C., McLeod M.P., McPherson D. K., Mattei B., MoIntosh T.C., McLeod M.P., McPherson D.L., RA Mont S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Pittman G.S., Pan M.S., Pollard J., Purl V., Resee M.G., Rahenrt K., Remington K.A., Nusskern D.R., Parle D.J.M., Rahenrt K., Remington K., Sunders R.D.C., Scheeler F., Shen H., RA Suler E., Spradling A.C., Stapleton M., Strong R., Sun E., Steralling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun S., Wallsams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O., Zheng X.H., Zhong F.N., Zhong W., Zhu X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";

REMI, Agong F.R., Zhong F.N., Zhong W., Zhu X., Zhu X., Smith R. Schence 287:285-2155(2000).

F. Fybase; Fbgn0030203; CG13303.

SEQUENCE 122 AA; 13139 WW; EF8D5468CFDE8BEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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J. Leukoc. Biol. 0.0-0(2000).
Leukoc. Biol. 0.0-0(2000).
Interpro; IPR001304;
Interpro; IPR001304;
Interpro; IPR001351;
PR00159; lectin_c;
PRINTS; PR00059; Lectin_c;
PRONTITE; PR00170; EMAJORBASICP
PROSTITE; PS000615; C_TYPE_LECTIN_1; 1.
SMART; SM00034; C_LECT; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
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Macias M.P., Welch K.C., Denzler K.L., Larson K.A., Lee N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 122;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
EOSINOPHIL MAJOR BASIC PROTEIN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%; Score 31; DB 71.4%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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SEQUENCE FROM N.A.
STORT./6J; TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 71.4 ses 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 AA;
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25 EAPGSRH 31
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Length 222;

DB 11; 75;

Score 31; Pred. No.

79.5%; 85.7%;

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SEQUENCE
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                                                                                                                                                                                                                                                           09MA16;
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                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                      "A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, ALO31184; AA20190.1; -.
InterPro; IPR002502; -.
Pfam: FF01510; Amidse_2: 1.
Hypothetical protein.
SEQUENCE 242 AA; 26018 MW; 6DD10FF18A2EC544 CRC64;
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum
Kinashi H., Hopwood D.A.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INTERLEUKIN-1 RECEPTOR ASSOCIATED PROTEIN KINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.5%; Score 31; DB 2; Length 242; 71.4%; Pred. No. 81;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                     Murphy L., Harris D.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAX-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 26.0 KDA PROTEIN.
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1;
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Mismatches
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                                                                                           PRT;
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Conservative
                                                                                          PRELIMINARY;
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                                                                                                                                                                Streptomyces coelicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=A3(2);
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                              NCBI_TaxID=1902;
                                      61 EVEGSQH 67
                  1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVPGSQH 7
                                                                                                                                                                                                                          STRAIN-A3(2);
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                                                                                         086582
086582;
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                                                                      19
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Matches
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Q9QY63
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SEQUENCE FROM N.A. Checks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Conn L., Conway A., Ganzalez A., Hansen N., Howing B., Koo T., Lam B., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome
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Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                           Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
and mouse reveals new untranslated sequences.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF121351; AF122115.1; -.
MGD; MGI:107420; Illrak.
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO10793; AAF681106.1;
SEQUENCE 260 AA; 29128 WW; B149F22073AA0B92 CRC64;
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                                                                                                                                                                                                                                                                                                        ED22D000546F0E88 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
82;
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                                                                                                                                                                                                                                             ATP-binding, Kinase, Receptor, Transferase.
NON_TER 243 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                     InterPro; IPR000719; -...
Pfam; PF00069; pkinase; I.
PROSITE; PS00107; PROTEIN_KINASE_ATF; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                           Score 31;
Pred. No.
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                                                                                                                                                                                                                                                                                                        26539 MW;
                                                                                                                                                                                                                                                                                                                                                                                           79.5%;
83.3%;
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                                                                                                                                                                                                                                                                                                     243 AA;
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Best Local Similarity
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Serine esterase.
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SEQUENCE
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MEDLINE-20504483; PubMed=11016950;
MG W.V., Kennedy S.P., Mahalras G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Ballaa N.S., Thorsson V., Sbrogna J.,
Swartzall S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Dansiels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-99051329, PubMed-9831651,
Chan H.Y.E., Harris S.J., O'Kane C.J.;
"Identification and characterization of kraken, a gene encoding
putative hydrolytic enzyme in Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                         Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE SERIME HYDROLASE (EC 3.1.-.-) (KRAKEN PROTEIN).
KRAKEN OR CG3943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL; AE005096; AAG20195.1; -.
SEQUENCE 274 AA; 29944 MW; 2BE706911A76CD3D CRC64;
                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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Matches 5; Conservative
                                                                                                                                                    PRELIMINARY;
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                         :111 ||
66 KVPGKOH 72
1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                       Halobacterium
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DT 01-JAN
DT 01-MAN
DT 01-M
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                                                                                                           RESULT 22
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ABSTRACTOR G.C., Mortuman D.R., Yanddall N.D., Ihango N.C., Chen L.D.,
Ran Ran, R.D., C., Mortuman D.K., Millades N.C., Changeo N., Pfeliffer B.D.,
Ran Ran, K.B., Pold-C.C., Baxter E.G., Half C., Melanow C.R., Millado G.L.G.,
Abrill S.F., Adopsyon A., An H.-J., Andrews-Fennicche L., Banddwin D.,
Ran Ballow R.W., Benose P.V., Berman B.P., Bhanddari D., Bolshabov S.,
Ran Borkova D., Relence P.V., Berman B.P., Bhanddari D., Bolshabov S.,
Ran Gerry J.W., Carley S., Danhle C., Powenbort L.B., Patilse P. M.,
Ran Cherry J.W., Barley S., Danhle C., Powenbort L.B., Patilse P. M.,
Ran Dutin K.J., Barupe D.R., Balley R. M., Cadisu E., Center A., Chandre I.,
Ran Dutin K.J., Barupe D.R., Balley R. M., Chassen K. A.
Ran Dutin K.J., Barupe D.R., Balley R. J., Weshport L.M., Indexton B.P., M.,
Ran Dutin K.J., Barupe D.R., Balley R. S., Gelbart W.M., Glasser K.,
Ran Glodek A., Good F., Gorell J.H., Gu Z., Guan P., Marchia M., Chandre J. M., Marthylov L., Marry D., Helman T.J., Hermandez J.R., Bouck J.,
Randolf M., Watter B., McKincoh T.C., Percent S., Patilson D.L.,
Randolf M., Watter B., McKincoh T.C., McIncod H.P., Webberson D.-N.,
Randolf M., Watter B., Watter M. Watter B., Weather F., Shan B., C.,
Randolf M., Watter B., Watter G., Percent P., Webberson D.-N.,
Randolf M., Watter B., Watter G., Percent F., Shan B., C.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Watter B., Wang A.H., Wang A.H.,
Randolf M., Watter B., Wang A.H., Wang A.H.,
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                                                                                                                                                                                                    White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann K.E., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 41.6 KDA PROTEIN.
Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
                                                                                                                   Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee J.S., Kang H.S.; "Sequence analysis of 65G3 cosmid clone of Zymomonas mobilis ZM4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.5%; Score 31; DB 2; Length 353; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 0; Indels
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF088897; AAF18289.1; -.
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PROSITE; PSO0557; FENA, HYDROXY_ACID_DH; 1.
SROHFNCE 353 AA; 37877 MW; 14FB78FAEZE18C8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000139; -. ProDom; PP005042; -; 1. ProDom; PP005242; -; 1. Hypothetical protein. SEQUENCE 371 AA; 41559 WW; 8D519E1509BAB64F CRC64;
                          353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 371 AA
PRT;
                                                                                                                                                                             STRAIN=R1;
MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                         Science 286:1571-1577(1999).
EMBL; AE001954; AAF10604.1;
HSSP; P05414; 1GOX.
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Best Local Similarity 83.3
Matches 5; Conservative
PRELIMINARY;
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                                                                                                    Deinococcus radiodurans.
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                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=542;
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                                                                                                                                                                                                                                                                                                 Fraser C.M.;
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Q9RH15;
                                                                                   DR1031
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Oy 2 VPGSQH 7
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Db 288 LPGSQH 293
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Search completed: July 16, 2001, 16:43:36 Job time: 470 sec

Sequence:

Run on:

Searched:

Database

Result Š

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Sequence Seq
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APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOSSMORE, Sheena
APPLICANT: Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
ITLE CO INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
STREFF.
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US-08-209-521-30

US-08-961-810-133

US-08-961-82-133

US-08-952-902D-133

US-08-952-902D-133

US-09-073-354-1

US-09-073-359-1

US-09-133-259-1

US-09-1418-027-1

US-09-361-095-1

US-08-96-925-4

US-08-96-925-4
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US-08-709-177-35
US-08-833-678A-3
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APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AGG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: STEMART, Michael I.
REGISTRATION NUMBER: 24,973
RETERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08292968 Patent No. 5856122 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 93 amino acids TYPE: amino acid
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abbana
STREET: Surr
CITY: Toronto
      Patent No. 5223610
Sequence 2, Appli
                                                                                                                                                                                                            July 16, 2001, 16:36:18; Search time 30.3 Seconds (without alignments) 13.962 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 5, Sequence 5, Sequence 2, Sequence 2, Sequence 2, Sequence 21, Sequence 21, Sequence 21, Sequence 21, Sequence 2, Sequence 2
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Sequence 12,
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Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-467-976-26
US-08-467-976-26
US-08-082-514-26
US-08-92-337-5
US-08-952-337-6
US-08-972-171-2
US-08-972-171-2
US-09-101-07-2
US-09-101-07-2
US-09-101-07-2
US-09-101-07-2
US-08-952-1376-21
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US-08-222-715B-27
US-08-709-784-2
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US-09-027-337-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                    APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: MAZES, Bart
APPLICANT: MAZES, Bart
APPLICANT: MAZES, BART
ATTILE OF INVENTION: MODIFICATION OF PERFUSSIS TOXIN
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 107; DB 2; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                    Sequence 26, Application US/08467536 Patent No. 5977304
                        1 GETFQVEVPGSQHIDSQKKAI 21
                                                               35 GETFQVEVPGSQHIDSQKKAI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSEE: Sim & MCE
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STRANDEDNESS: sin
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                                                                                                                                                                                                              GENERAL INFORMATION:
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TOPOLOGY:
US-08-467-536-26
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US-08-467-976-26
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                                                           Query Match 100.0%; Score 107; DB 2; Length 93; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STEIN, Penelope E.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: HAZES, BATT
TILE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SCOURNES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBULINEY
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/467,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE-POCKET NUMBER: 1038-454 MIS:vg
TREECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/08467974 Patent No. 5965385 GENERAL INFORMATION:
                                                                                                                                                                           35 GETFOVEVPGSQHIDSOKKAI 55
                                                                                                                                                   1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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Best Local Similarity
Matches 21; Conserva
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US-08-467-974-26
US-08-292-968-26
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Sequence 6, Application US/08829026A
Sequence 6, Application US/08829026A
Patent No. 5837825
GENERAL INFORMATION:
APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Janelle S. Graeter
STREET: Room 411, Building 005, BARC-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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COUNTRY: USA
ZIE: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
TITING DATE: 18-AUG-1997
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END PC compatible
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,514
FILING DATE:
PRIOR APPLICATION DATA:
PROBLICATION NUMBER: US 08/292,968
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CANNEY/AGENT INFORMATION:
NAME: CANNEY/AGENT INFORMATION:
NAME: CANNEY/AGENT INFORMATION:
                           APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SOUGHNES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 107; DB 4;
100.0%; Pred. No. 2.2e-11;
iive 0; Mismatches 0;
                                                                                                                    ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
    APPLICANT: ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 GETFQVEVPGSQHIDSQKKAI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                       STATE: Ontario
COUNTR: Canada
ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                STREET: 6tn ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-829-026A-6
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                                                           APPLICANT: STEIN, Penelope E.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LAOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ALZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Sulte 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 107; DB 3;
100.0%; Pred. No. 2.2e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1038-453 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROCR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   STREET: Suite 701, 330 University
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/467,976
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-082-514-26
US-09-082-514-26
Sequence 26, Application US/09082514
Fatent No. 6168928
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, RAYMOND P.
APPLICANT: KLEIN, MICHEL H.
Sequence 26, Application US/08467976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 595-1155
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 GETFQVEVPGSQHIDSQKKAI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.
Matches 21; Conservative
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US-08-467-976-26
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Length 102;

Score 101; DB 3; L Pred. No. 2.7e-10; 0; Mismatches 1;

0; Mismatches

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EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 102
TYPE: PRT
                                                                                                                                                                                                                                                                                                                1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                        44 GATFQVEVPGSQHIDSQKKAI 64
                                                                                                                                                                                                                               94.4%;
95.2%;
                                                                                                                                               ; ORGANISM: Escherichia coli
US-08-952-337-6
                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & STREET: 330 Univ CITY: Toronto STATE: Ontario
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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REPERBENCE: 3846/0D/58
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER PILING DATE: 1996-01-05
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1996-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASELED FOR Windows Version 3.0
SEQ ID NOS: 6
SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                    Length 371;
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APPLICANT: Holmgren, Jan
APPLICANT: Holmgren, Jan
APPLICANT: Holmgren, Jan
TILLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: BYTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/D0758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
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95.2%; Pred. No. 2.7e-10;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                  100.0%; Score 107; 100.0%; Pred. No. 1
                                                                  0106.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-952-337-5; Sequence 5, Application US/08952337; Patent No. 6019973
                       NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-566
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08952337 Patent No. 6019973
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 GETFOVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                          : 371 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Vibrio cholerae
US-08-952-337-5
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 21; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 20; Conservi
                                                                                                                                                                                                                                                                        US-08-829-026A-6
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Sequence 2, Application US/08472171

Patent No. 5932714

GENERAL INFORMATION:
APPLICANT: LOSSMOCE, Sheena M.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Application Michel H.
TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/472,171 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 RFICH APPLICATION DATA: APPLICATION NUMBER: US 08/393,334 FILING DATE: 23-FEB-1995 ATTORNEY/SEPT IN NUMBER: US 08/393,334 FILING DATE: CATORNEY/SEPT IN NUMBER: US 08/393,334 FILING DATE: CATORNEY/SEPT IN NUMBER: US 08/393,334 FILING DATE: US 08/393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 2;
Pred. No. 2.8e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sim & McBurney
330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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REGISTRATION NUMBER: 10;
REFERENCE/DOCKET NUMBER: 10;
TELECOMMUNICATION: TELEPHONE: 416-595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 95.23
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416-595-1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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US-09-374-597-2

Sequence 2, Application US/09374597

Patent No. 6140082

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M.

APPLICANT: Yacoob, Reza K.

APPLICANT: Zealey, Gavin R.

APPLICANT: Riein, Michel H.

TITLE OF INVENTION: Expression Of Gene Products From

TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella

NUMBER OF SEQUENCES: 56

CORRESPONDENCE: Sim & MCBULNEY

STREET: 330 University Avenue, 6th Floor
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.4%; Score 101; DB 2;
95.2%; Pred. No. 2.8e-10;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION WOMBER:
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION WOMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1153
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GETFQVEVPGSQHIDSQKKAI 21
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amino acid
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COUNTY: Canada
ZIP: M5G 1R7
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
    STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toronto
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-013-047-2
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                                                                                                                                                                                             APPLICANT: LOOSMOTE, Sheena M
APPLICANT: Yacoob, Reza K
APPLICANT: Yacoob, Reza K
APPLICANT: Zacoob, Reza K
APPLICANT: Zacoob, Reza K
APPLICANT: Zacoob, Reza K
APPLICANT: Zacoob, Richel H
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE SIM & MCBUTNES;
ADDRESSEE: SIM & MCBUTNES;
STATE: OTHERIO
STATE: OTHERIO
COUNTRY: Canada
ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
ATTORNES/AGENT INFORMATION:
NAME: Stewart Michael IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09013047
Patent No. 5998168
CENERAL INFORMATION:
APPLICANT: LOSORNICE, Sheena M.
APPLICANT: Acaley, Gavin R.
APPLICANT: Xealey, Gavin R.
APPLICANT: Alein, Michel H.
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & Medurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1038-724 MIS: jb
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    Sequence 2, Application US/08894526
Patent No. 5942418
GENERAL INFORMATION:
45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 GATEQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 103 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-894-526-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toronto
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                                                                                                            US-08-894-526-2
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Gaps

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Length 103; Indels

Gaps

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RESULT 14
PCT-US95-13376-21
; Sequence 21, Application PC/TUS9513376
; GENERAL INFORMATION:
    APPLICANT: The Texas A&M University System
    APPLICANT: The Texas A&M University System
    APPLICANT: Ollege Station, Texas 77843-3369
; TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
: CITY: Houston
94.4%; Score 101; DB 4; Length 103;
95.2%; Pred. No. 2.8e-10;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 103;
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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTERCOTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/00758
CURRENT APPLICAND NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 5; Length lu-
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
ELING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W.
REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36170/3P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
2IP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/08952337
; Patent No. 6019973
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                                                                                                                     45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                             1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.48;
95.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 713-850-0909
713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 103 amino acids
amino acid
                        Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.2
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-952-337-1
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    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tarig A. Hag
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 4; Length 10
Pred. No. 2.8e-10;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: USA
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,852
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100
                FILING DATE: FEBRUARY 23, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REMERENCE/DOCKET NUMBER: 1038-964
TELEPHONE: 416-595-1155
TELERAX: 416-595-1153
TELERAX: 055-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P01590US1
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Patent No. 6194560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fox, David L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
TELEFAX: 713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFRX: 713-651-522
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-374-597-2
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-191-852-21
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APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUPTER: USE 1210-1789
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
SOFFWARE: Patentin Rc-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.4%; Score 101; DB 2;
95.2%; Pred. No. 3.5e-10;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                        11526.1-US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/449,045C
FILING DATE: 24-MAY-1995
                                                                                                                  APPLICATION NUMBER: US/08/747,410 FILING DATE: 12-NOV-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAX-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/08449045C; Patent No. 5770203; GENERAL INFORMATION:
                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 1152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 GATFQVEVPGSQHIDSQKKAI 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HATT-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE: US-08-747-410-2
       MEDIUM TYPE:
COMPUTER: IE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-449-045C-4
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; Sequence 2, Application US/08747410
; Patent No. 5993820
; GENERAL INFORMATION;
; APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
; TITLE OF INVENTION: CHIMERIC LTB VACCINES
; TITLE OF INVENTION: CHIMERIC LTB VACCINES
; MUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 5993820west Center, 90 South Seventh St
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HOLMGren, Jan
APPLICANT: Lebens, Michael R.
TILLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1996-05-02
EARLIER APPLICATION NUMBER: ES 9501682-0
EARLIER APPLICATION NUMBER: ES 9501682-0
EARLIER FILING DATE: 1995-05-05
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 2
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.4%; Score 101; DB 3; Length 123; illarity 95.2%; Pred. No. 3.4e-10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                  Length 123;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                           / Match 94.4%; Score 101; DB 3;
Local Similarity 95.2%; Pred. No. 3.4e-10;
nes 20; Conservative 0; Mismatches 1
EARLIER APPLICATION NUMBER: PCT/SE96/00570 EARLIER FILING DATE: 1996-05-02 EARLIER APPLICATION NUMBER: SE 9501682-0 EARLIER OF SEQ ID DATE: 1995-05-05 SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-952-337-2; Sequence 2, Application US/08952337; Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GATFQVEVPGSQHIDSQKKAI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 GATFQVEVPGSQHIDSQKKAI 85
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US-08-952-337-2
                                                                                                                                                                                                                 ORGANISM: Vibrio cholerae US-08-952-337-1
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Matches 20; Conserv
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                                                                                                                                          SEQ ID NO 1
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-747-410-2
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Best Local S
Matches 20
                                                                                                                                                                                             TYPE: PRT
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Gaps

us-09-786-648-5.rai

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Patent No. 5223610
Patent No. 5223610
Patent No. 100 Frank H.; Sutcliffe, Gregor
TITE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
HOWBORD PROWOTER
NUMBER OF SEQUENCES: 18
PAPELICATION DATA:
PILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                   Ouery Match 83.2
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS: si
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                                                                                                                                                                                                   ; LENGTH: 124
5223610-3
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    5223610-3
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APPLICANT: Burnette, W. Neal
APPLICANT: Barnette, W. Neal
APPLICANT: Raslow, Harvey R.
ATTLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Qaks
                                                                                                                                                                                                                                                                                Query Match 83.2%; Score 89; DB 1; Length 124; Best Local Similarity 85.7%; Pred. No. 4e-08; Matches 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.2%; Score 89; DB 2; Length 124;
85.7%; Pred. No. 4e-08;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/435,605A FILING DATE: 05-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08435605A Patent No. 5874287
                                       NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-19
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INPORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFRENCE/CDCKET NUMBER: A-19.
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                         1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 GAIFQVEVPSSQHIDSQKKAI 86
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FILING DATE: 06-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 83.2
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-605A-12
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STATE: California
COUNTRY: USA
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STRANDEDNESS: sir
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US-08-435-605A-12
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RESULT 20

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Length 124;
                                                                                              3; Indels
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: APPLICANT: Lal, Preeti
APPLICANT: Lal
); DB 6;
0. 4e-08;
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SOFTWARE: FASTEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
                                                                                              Mismatches
Score 89;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                    66 GAIFQVEVPSSQHIDSQKKAI 86
83.28;
                                                                                                                                                                                                  1 GETFQVEVPGSQHIDSQKKAI 21
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
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269 GQSINVHTPNSQKVDSQKAA 288

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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Taninoto, Hirotoshi
TITLE OF INVENTION: TANG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
                                                                                                  Sequence 4, Application PC/TUS9511684
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TILLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
TILLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: The Scripps Research Institute, Office of ADDRESSE: Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/Near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: BEC0019P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09027337B
; Patent No. 5972616
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: 1ELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEC ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 1810 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein PCT-US95-11684-4
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                                                                                                                                                                                                                                                                                                                               La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1. CLASSIFICATION:
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                                                                RESULT 23
PCT-US95-11684-4
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LENGTH: 855
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                                                                                 50.5%; Score 54; DB 2; Length 448; 50.0%; Pred. No. 0.21;
                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KIRASES NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFRAME: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0321 US
                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09272796
Patent No. 6207148
GAPPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Clay, Neil C.
APPLICANT: Gugler, Karl G.
APPLICANT: Glay, Neil C.
APPLICANT: Glay, Neil C.
APPLICANT: Glay, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                          269 GQSINVHTPNSQKVDSQKAA 288
                                                                                                                                                                1 GETFQVEVPGSQHIDSQKKA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GETFQVEVPGSQHIDSQKKA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                    Best Local Similarity 50.0 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TELYNOTO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIA.
LIBRARY: TEL.
; CLONE: 40194
US-08-878-989-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                   RESULT 22
US-09-272-796-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-272-796-2
                                                                                 Query Match
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Pred. No. 1e+02;

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                                    Amino acid sequence of TADG-15 encoded by nucleotides 23\ \text{to }2589\ \text{of Sequence }1
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: PERLER, FRANCINE B.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: SOUTHWORTH, MAURICE W.
APPLICANT: SOUTHWORTHON: RECOMBINANT THEROMSTABLE DNA POLYMERASE
TITLE OF INVENTION: FROM ARCHAEBACTERIA
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STREET: MASSACHUSETTS
COUNTRY: US
                                                                                                                                                         Score 42; DB 2; Length 855;
Pred. No. 54;
                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/811,421
FILING DATE: 18-DEC-1991
PRIOR APPLICATION NUMBER: US 07/686,340
FILING DATE: 17-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
RESISTRATION NUMBER: 30901
RESISTRATION NUMBER: 30901
RESISTRATION NUMBER: NEB-101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08271364A Patent No. 5756334
                                                                                                                                                           39.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
                                                                                                                                                         Query Match
Best Local Similarity 50.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-271-364A-8
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                               367 TWNIEVPNNQHV 378
                                                                                                                                                                                                                                       3 TFQVEVPGSQHI 14
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                                      CTHER INFORMATION:
CTHER INFORMATION:
Patent No. 5972616
US-09-027-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino a STRANDEDNESS:
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US-08-271-364A-8
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38.3%; Score 41; DB 1; Length 1022;

Query Match

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Gaps
         ;
0
          5; Indels
         Mismatches
Best Local Similarity 46.7%;
Matches 7; Conservative
                                         1 GETFQVEVPGSQHID 15
                              οy
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Search completed: July 16, 2001, 16:36:18 Job time: 207 sec

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Compugen Ltd
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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OM protein - protein search, using sw model

July 16, 2001, 16:37:02; Search time 34.9 Seconds (without alignments) 45.836 Million cell updates/sec Run on:

US-09-786-648-5 107 Perfect score: Title:

1 GETFQVEVPGSQHIDSQKKAI 21 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 219241 seqs, 76174552 residues Searched:

219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heat-labile entero	cholera enterotoxi	hypothetical prote	RAD23 protein homo	hypothetical prote	hypothetical prote	kinesin heavy chai	genome polyprotein	conserved hypothet	hypothetical prote	probable carnitine	genome polyprotein	probable receptor-	ubiquitin / riboso	ubiquitin / riboso	ubiquitin 18 - sli	ubiquitin (clone l	hypothetical prote			polyubiquitin 5 (c	polyubiquitin 7 (c	tenascin precursor	probable peptide c	stress-activated p	hypothetical prote	chorismate synthas	4-aminobutyrate tr	probable peptide c
SUMMARIES	ID	QLECB	XVVCB	A86457	T04150	C96580	C86400	T49189	S15760	S78364	T19866	T49574	VFIHJH	C84726	UQDOR	UQDOR7	D34080	B27806	T04861	C34080	B34080	A27806	A34080	A32230	E82963	JC5694	S76110	S17246	JC4022	E85512
	DB	-	-	~	~	7	7	~	7	7	7	~	П	7	—	Т	7	7	~	~	~	7	~	П	~	~	7	-	7	7
	Query Match Length	124	124	255	392	91	574	439	2733	263	374	864	2731	641	128	154	228	229	368	380	380	381	532	1810	204	427	1742	376	200	166
dР	Query	100.0	88.8	45.8	43.9	43.0	43.0	42.1	42.1	41.1	41.1	41.1	41.1	40.7	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	39.3	39.3	39.3	38.8	38.8	38.3
	Score	107	95	49	47	46	46	45	45	44	44	44	44	43.5	43	43	43	43	43	43	43	43	43	43	42	42	42	41.5	41.5	41
	Result No.	1	2	Э	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

translation releas protein F20B17.2 [pertussis toxin ch	yaan protein - Bac queuine tRNA-ribos hypothetical prote	repressor protein inner membrane pro pyruvate carboxyla	zinc finger protei DNA-directed DNA p hypothetical prote	conserved hypothet mutL protein homol translation initia ubiquitin / riboso
E64748 C96827 A25973	S66056 T46898 T01770	S01433 G81692 A83978	T34020 S42459 T20566	D81715 S47598 H72513 UQNCR
224	777	000	000	1555
166 260 269	386 399 550	683 787 1150	1167 1702 2911	374 862 148 149
38.3	888	38.33		37.9 37.9 37.4 4.7
4 4 4 1 1 1 1	444	4 4 4	444	40.5 40.5 40
30 31 32	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	37 38 38	4 4 4 9 0 1	4 4 4 4 2 6 4 6

ALIGNMENTS

RESULT

RESULT 1	
OLECB .	
heat-labile enterotoxin chain B precursor - Escherichia coli	
C; Species: Escherichia coli	
C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999	
C; Accession: A01820; B26946; I41194; I41287; I67644; A61475	
R;Dallas, W.S.; Falkow, S.	
Nature 288, 499-501, 1980	
A; Title: Amino acid sequence homology between cholera toxin and Escherichia coli heat	1i heat
A;Reference number: A01820; MUID:81074965	
A; Accession: A01820	
A; Molecule type: mRNA	
A; Residues: 1-124 <dal></dal>	
R;Yamamoto, T.; Gojobori, T.; Yokota, T.	
J. Bacteriol. 169, 1352-1357, 1987	
A; Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichi	herichi
A; Reference number: A26946; MUID:87137303	
A; Accession: B26946	
A; Molecule type: DNA	
A; Residues: 1-27, 'E', 29-63, 'K', 65-124 < YAM>	
A; Cross-references: EMBL:M15363; NID:9148335; PIDN:AAA24792.1; PID:9148336	
R; Leong, J.; Vinal, A.C.; Dallas, W.S.	
Infect. Immun. 48, 73-77, 1985	
A:Title: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons	strons

A;Title: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons A;Reference number: 141194; MUID:85156481

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-5, 'F', 7-17, 'C', 19-24, 'S', 26-27, 'E', 29-33, 'H', 35-63, 'K', 65-66, 'A', 68-122 A; Cross-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831 A; Experimental source: plasmid ENT-R PCG86 R; Ibrahimi, I.; Gentz, R. J. Biol. Chem. 262, 10189-10194, 1987 A; Title: A functional interaction between the signal peptide and the translation appa

ticulum. A;Reference number: 141287; MUID:87280041 A;Accession: 141287 A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-22 <RE2>

A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
FEMS Microbiol. Lett.. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic A;Reference number: 153542; MUID:93252225

A, Accession: 167644 A, Status: preliminary; translated from GB/EMBL/DDBJ

A; Modecule type: DNA A; Residues: 1-17, C', 19, 'Y', 21-24,'S', 26-27,'E', 29-63,'K', 65-66,'A', 68-122,'E', 124 <R A; Cross-references: GB:S60731; NID:g408994; PIDN:AAC60441.1; PID:g408996 R; Tsuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.; Microb. Pathog. 2, 381-390, 1987

```
R:Dams, E.; de Wolf, M.; Dierick, W.
Biochim. Biophys. Acta 1090, 139-141, 1991
A:Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A:Reference number: S17665; MUID:91355224
A:Rolecule type: DNA
A:Rolecule type: DNA
A:Rolecule type: TS8785; MID:94888; PIDN:CAA41591.1; PID:948890
B:Ma. O.J.: Liu, C.X.; Xiony, L.S.; Yu, X.O.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 34, 274-280, 1991
A:Title: B subunit of cholera toxin produced in Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
A; Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
B; Takao, T.; Watanabe, H.; Shimonishi, Y.
B; Takao, T.; Watanabe, H.; Sols-508, 1985
A; Title: Pacile identification of protein sequences by mass spectrometry.
A; Reference number: A21910; MUID:85126976
                                                                                                                                                                                                                                                                                                                                                                                        A. Molecule type: protein
A. Residues: 22-38, "H', 40-41 < MAQ>
R. McAture 306, 531-557, 1983
A. Reference number: A93320; MUID:84068199
A. Accession: A05130
A. Molecule type: DNA
A. Residues: 1.32, "S', 34-74, "S', 76-124 < MEK>
A. Crossion: An an area of a molecule type: DNA
A. Residues: 1.32, "S', 34-74, "S', 76-124 < MEK>
A. Cross references: GB: X00171; NID:948347; PIDN:CAA24996.1; PID:9758351
A. Cross y, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A. Title: Covalent structure of the beta chain of cholera enterotoxin.
A. Reference number: A01819; MUID:78005537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>
A; Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>
A; Note: the difference at residue 70 may be due to deamidation during preparation
R; Nakashima. Y.; Nathorokowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
A; Title: Primary structure of the B subunit of cholera enterotoxin.
A; Reference number: A38034; MUID:77026365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 252, 7249-7256, 1977
A;Title: Determination of the primary structure of cholera toxin B subunit.
A;Reference number: A38033; MUID:78005536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Map position: 1
C;Complex: the cholera enterotoxin molecule contains three kinds of chain C;Complex: the cholera enterotoxin molecule contains three kinds of chains ciate noncovalently with the subunit B, an aggregate of five beta chains C;Function:
A;Description: involved in binding of the toxin to cell membranes
A;Description: involved in binding of the toxin to cell membranes
C;Superfamily: cholera enterotoxin beta chain
E;1-21/Domain: signal sequence #status predicted <NGC>
F;22-124/Product: cholera enterotoxin chain B #status predicted <MAT>
F;30-107/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for residue 33 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 22-38, H',40-42, 'N',44-67, 'T',69-90,'N',92-124 <TAK>
A;Residues: 22-38, H',40-42, 'N',44-67, 'T',69-90,'N',92-124 <TAK>
A;Experimental source: biotype Inaba 569B
A;Note: Asn-65 was partially deaminated to Asp
C;Comment: The authors translated the codon TCA for residue 33 as C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 22-38, 'H',40-42,'N',44-67,'T',69-90,'N',92-124 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 4e-08;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
                                                                                                                                                                                                                                                                                                                                       A; Reference number: PC1010
A; Accession: PC1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A21910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A01819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A38034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A38033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Lai, C.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin isol
A;Reference number: A61475; MUID:89180953
                                                                                                                                                                                                                                                     a
                                                                                                                                                                                       щ
                                                                                                                                                                                                                                           of the toxin is produced by the A chain, which
                                                                                                                                                                                 Complex: the heat-labile enterotoxin molecule contains one A chain and five or six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                             A.Accession: AG1475
A.Molecule type: protein
A.Rocession: A61475
A.Molecule type: protein
A.Rocessides: 22-24, S', 26-27, E', 29-63, K', 65-66, A', 68-95, A', 97-122, E', 124
A.Rocesidues: 22-24, S', 26-27, E', 29-63, K', 65-66, A', 68-95, A', 97-122, E', 124
A.Rocesidues: 22-24, S', 26-27, E', 29-63, K', 65-66, A', 68-95, A', 97-122, E', 124
A.Rocesidues: actain 240-3
A.Rocesidues: the heat-labile enterotoxin molecule contains one A chain and five
C.Superfamily: cholera enterotoxin beta chain
C.Superfamily: cholera enterotoxin beta chain
C.Superfamily: signal sequence #status predicted <SIG>
F:1-2.14/Product: heat-labile enterotoxin chain B #status predicted <MAT>
F:30-107/Disulfide bonds: #status predicted
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A; Accession: JC1078
A; Molecule type: DNA
A; Residues: 1-20, '0', 22-31,'0', 33-38,'H', 40-49,'G',51-67,'T',69-124 <SHI>A; Experimental source: classical biotype strain 569B
                                                                                                                                                                                                                                                                                                   'Keywords: enterotoxin
12.1/Domain: signal sequence #status predicted <SIG>
12.11A/Product: heat-labile enterotoxin chain B #status predicted
30-107/Disulfide bonds: #status predicted
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100.0%; Pred. No. 4.6e-10;
tive 0; Mismatches 0;
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Matches 21; Conservative
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hypothetical protein AAD45990.1 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Grado) (Species: Grado)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96580 C;Accession: C96580 C;Accession: C96580 C;Accession: C96580 C;Accession: C96580 C;Accession: Cohor, L; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000 A;Authors: Hunter, J.C.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE005173; NID: 94587538; PIDN: AAD25769.1; GSPDB: GN00141
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NyAlternate names: protein MAA21.110
C.Species: Arabidopsis thaliana (mouse-ar cress)
C.Species: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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Pred. No. 18;
2; Mismatches
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Best Local Similarity
'-hag 10; Conserva
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Best Local Similarity
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                                                                                                                                                                                                      Dypothetical protein AAG21605.1 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C. Species: A. S. Botter, J. R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Anthors: Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 (A. A. Li, Y.; Liu, X.; Liu, X.; Liu, X.; Liu, X.; Liu, X.; Liu, Z.A.; Lurcos, J.S.; Majkin, E.; Kim, C. C.A.; Li, T.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Lurcos, J.S.; Maiti, R.; Marziali, A. Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A. Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A. A. Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
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C;Genetics:
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A;Molecule type: mRNA
A)Residues: 1-392 <SCH>
A;Cross-references: EMBL:U63530; NID:g1488296; PIDN:AAB65841.1; PID:g1488297
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C;Species: Oryza sativa (rice)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
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A;Gene: RAD23
C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
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hypothetical protein F1511.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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R; Schultz, T.F.; Quatrano, R.S.
Plant Mol. Biol. 34, 557-562, 1997
A; Title: Characterization and expression of a rice RAD23 gene.
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45.0%; Pred. No. 2.4;
tive 4; Mismatches
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A; Accession: T04150
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       101 ETFRVSGPGGQHRNKRDSAV 120
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Best Local Similarity 45.0°
Matches 9; Conservative
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Best Local Similarity 42.99
Matches 9; Conservative
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A; Residues: 1-255 <STO>
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C;Accession: T49574
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49574
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 04-Mar-2000
C;Accession: T19866
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A;Introns: 44/2; 95/1; 178/1; 234/3; 348/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C40H5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1.864 <SCH>
A; Cross-references: EMBL:AL355930; GSPDB:GN00116; NCSP:B208.220
A; Experimental source: BAC clone B208; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C40H5.3 - Caenorhabditis elegans
A;Genome: chloroplast
C;Superfamily: conserved hypothetical protein HI0188
C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Status: preliminary, translated from GB/EMBL/DDBJ A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1996
A;Reference number: 219189
A;Accession: T19866
                                                                                                                                                                               Score 44; DB 2
Pred. No. 16;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%; Score 44; DB 42.1%; Pred. No. 23; iive 2; Mismatches
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               30 ETVTLELPFSEHIEELKORL 49
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                                                                                                                                                                                   41.18;
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                                                                                                                                                 Ouery Match
Best Local Similarity 40.0*
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Best Local Similarity 42.1%
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-374 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Niconcains: RNA-directed RNA polymerase (EC 2.7.7.48)

Niconcains: RNA-directed RNA polymerase (EC 2.7.7.48)

C; Species: murine hepatitis virus, MHV
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000

C; Accession: S15760; S08652

R; Bredenbeek, P. J.; Pachuk, C. J.; Noten, A.F. H.; Charite, J.; Luytjes, W.; Weiss, S.R.; Nucleic Acids Res. 18, 1825-1832, 1990

A; Title: The primary structure and expression of the second open reading frame of the pc frameshifting mechanism.

A; Reference number: S15760; MUD: 90245573

A; Molecule type: genomic RNA
A; Residues: 1-2733 GBRE>
A; Cross-references: EMBL: X51939; NID: 958974; PID: 91334829

C; Superfamily: infectious bronchitis virus RNA-directed RNA polymerase
C; Keywords: nucleotidyltransferase; RNA biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conserved hypothetical protein 263 - Odontella sinensis chloroplast
C;Species: chloroplast Odontella sinensis
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
R;Kocssion: S78364
A;Atitle: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensia A;Accession: S78364
A;
                              R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000
A;Reference number: 225018
A;Accession: T49189
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 3
A;Introns: 39/3; 74/1; 97/3; 138/3; 147/2; 193/3; 200/2; 273/3; 304/2; 341/3; 401/3
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                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <RIE>
A;Cross-references: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.110
A;Experimental source: cultivar Columbia; BAC clone MAA21
C;Genetics:
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52.9%; Pred. No. 1.3e+02;
.ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.1%; Score 45; DB 2; Length 439; llarity 38.1%; Pred. No. 19; Conservative 4; Mismatches 9; Indels
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Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Gene: ATSP:MAA21.110
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Length 374;

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Length 864;

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C;Accession: E34080
R;Ohmachi, T.; Giorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostelium discoideum A;Reference number: A34080; MUID:89352609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:M23750; GB:J02858; NID:q167940; PIDN:AAA33264.1; PID:q167941
C;Superfamily: ubjquitin / rat ribosomal protein S27a; ribosomal protein S27a homolog
C;Keywords: protein biosynthesis: protein degradation; ribosome
F;1-76/Product: ubjquitin #status predicted <MAT1>
F;1-76/Domain: ubjquitin hamology <GBHS
F;7-154/Product: ribosomal protein S27a *status predicted <MAT2>
F;102-152/Domain: ribosomal protein S27a homology <RIB>
                                                                                                                                                                                                                                                                A;Title: Complete cDNA sequence of a Dictyostelium ubiquitin with a carboxy-terminal A;Reference number: S00357; MUID:88152253 A;Accession: S00357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: DUB1
C;Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology;
C;Keywords: DNA binding; protein biosynthesis; protein degradation; ribosome; zinc f
F;1-76/Poroduct: ubiquitin #status predicted <UBI>
F;1-76/Domain: ubiquitin homology <UBH>
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                                                                                      N'Alternate names: ubiquitin fusion protein
C;Species: Dictyostellum discoideum
C;Deccies: Dictyostellum discoideum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C;Accession: S00357; A2586
R;Mueller Taubenberger. A.; Westphal, M.; Jaeger, E.; Noegel, A.; Gerisch, GFEBS Lett. 229, 273-278, 1988
                                                             ubiquitin / ribosomal protein CEP52 - slime mold (Dictyostellum discoideum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Dictyostelium discoideum
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
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C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 23-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A;Residues: 1-128 <MUE>
A;Cross-references: EMBL:X07210; NID:g7381; PIDN:CAA30183.1; PID:g7382
A;Experimental source: strain AX2-214
C;Genetics:
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F;77-128/Domain: ribosomal protein CEP52 homology <CPH>
F;95-114/Region: zinc finger CCC motif
F;121-128/Region: nuclear location signal
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13;
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Mismatches
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Pred. No. 1
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Pred. No.
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Best Local Similarity 42.>
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Best Local Similarity 42.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable receptor-like protein kinase [imported] - Arabidopsis thaliana cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84726
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Tille, Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: C84726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-641 <STO>
A;Cross-references: GB:AE002093; NID:94887748; PIDN:AAD32284.1; GSPDB:GN00139
A;Gene: AL5931880
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAccession: B38815
A; Molecule type: genomic RNA
A; Molecule type: genomic RNA
A; Molecule type: genomic RNA
A; Molecule type: 1-2731 < LEE>
A; Cross-references: GB:M55148; NID:g331851; PIDN:AAA46458.1; PID:g331853
A; Cross-references: GB:M55148; NID:g331851; PIDN:AAA46458.1; PID:g331853
A; Clee, H.J.; Shleh, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bag6
Virology 180, 567-582, 1991
A; Title: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the A; Reference number: A38547; MUID:9111976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                           C; Accession: B36815

R; Lee, H.J.; Shieh, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagd submitted to Genbank, February 1991

A; Description: The complete sequence (22 kilobases) of murine coronavirus gene 1 encodin A; Reference number: A36815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Contents: annotation
A;Note: neither nucleotide nor complete amino acid sequence is given
C;Comment: This protein may be translated as a la-1b polyprotein by a ribosomal frameshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Gene: 1b
C.Superfamily: infectious bronchitis virus RNA-directed RNA polymerase
C.Superfamily: infectious bronchidyltransferase; RNA blosynthesis
C.Keywords: glycoprotein; nucleotidyltransferase; RNA blosynthesis
F:269,304,785,1184,1287,1224,1842,2196,2575,2630,2645,2665/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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                                                                                                                                                                   N,Alternate names: 1b protein
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: murine hepatitis virus, MHV
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999
C;Accession: B36815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.1%; Score 44; DB 1; Length 2731; 69.2%; Pred. No. 1.9e+02;
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                                                                                                                                                    genome polyprotein 1b - murine hepatitis virus (strain JHM)
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Pred. No. 50;
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50.0%;
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541 QTFWADAPGDAKIDALRKA
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|1198 ETFONNVPNYOHI 1210
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Best Local Similarity
Matches 11; Conserv
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Matches
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Query Match 40.2 Best Local Similarity 42.9 Matches 9; Conservative

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C. Accession: B34000
R.Ohmachi, T.; Glorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 525-5231, 1989
Biochemistry 28, 525-5231, 1989
A. Title: Molecular organization of developmentally regulated Dictyostelium discoideum
A. Reference number: A34080; MUID:89352609
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-380 < CMNA
A. Residues: GB-M2348
A. Experimental source: strain B, clone DCUB19
C. Superfamily: polyubiquitin 5; ubiquitin homology
C. Superfamily: polyubiquitin 5; ubiquitin degradation
F.1-76/Product: ubiquitin #status predicted <UBI>F:1-76/Domain: ubiquitin homology <UBHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Ohmachi, T.; Giorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostelium discoideum
A;Reference number: A34080; MUID:89352609
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C:Species: Dictyostellum discoideum
C:Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 11-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.Alternate names: ubiquitin 19
C.Species: Dictyostelium discoideum
C.Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 11-Apr-1997
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    slime mold (Dictyostelium discoideum)

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                                                                                                 Length 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;77-152/Domain: ubiquitin homology CUBH2>
F;153-228/Product: ubiquitin %status predicted <UB3>
F;153-228/Promain: ubiquitin homology CUBH3>
F;229-304/Promain: ubiquitin %status predicted <UB4>
F;229-304/Promain: ubiquitin %status predicted <UB4>
F;329-304/Product: ubiquitin %status predicted <UB5>
F;305-380/Product: ubiquitin %status predicted <UB5>
F;305-380/Domain: ubiquitin homology CUB5>
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A;Experimental source: strain B, clone DCUB12
C;Superfamily: polyubiquitin 5; ubiquitin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB Pred. No. 35; 5; Mismatches
                                                                                                                                                             Mismatches
                                                                                                    Score 43;
Pred. No.
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                                                                                                                                                             6; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-380 <OHM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: C34080
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                  A; Note: F28A21.100
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B27806
ubiquitin (clone lambda229) - slime mold (Dictyostellum discoideum)
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 06-Feb-1998
C;Accession: B27806
R;Glorda, R.: Ennis, H.L.
Mol. Cell. Biol. 7, 2097-2103, 1987
A;Title: Structure of two developmentally regulated Dictyostellum discoideum ubiquitin gasterence number: A27806; MUID:87257921
A;Reference number: A27806; MUID:87257921
A;Residues: 1-229 cGIO>
A;Cross-references: GB:M23754
C;Superfamily: polyubiquitin 3; ubiquitin homology
C;Superfamil: ubiquitin homology cUBH1>
F;177-152/Domain: ubiquitin homology cUBH3>
F;153-228/Domain: ubiquitin homology cUBH3>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T04861
R;Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, B.; Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, A;Reference number: 215387
A;Reference number: 215387
A;Residues: 1-368 <ABEV
A;Coss.references: EMBL:AL035526
A;Experimental source: cultivar Columbia; BAC clone F28A21
C;Genetics:
A;Map position: 4
A;Introns: 282/2
C;Accession: D34080
R;Ohmachi, T.; Glorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 5226-5231, 1989
A;Title: Wolecular organization of developmentally regulated Dictyostelium discoideum u.A;Reference number: A34080; MuID:89352609
A;Title: Wolecular organization of developmentally regulated Dictyostelium discoideum u.A;Reference number: A34080; MuID:89352609
A;Accession: D34080
A;Accession: D34080
A;Essidues: preliminary
A;Molecule type: mRNA
A;Residues: 1-228 < OHM>
A;Cross-references: GB:M23751
C;Superfamily: polyubiquitin 3; ubiquitin homology
C;Reywords: duplication; nucleus; polyprotein; protein degradation
F;1-76/Domain: ubiquitin homology <UBH1>
F;77-152/Domain: ubiquitin homology <UBH3>
F;153-228/Domain: ubiquitin homology <UBH3>
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ed. No. 20;
Mismatches
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42.9%; Pred. No. 20;
Live 5; Mismatches
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Pred. No.
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Query Match 40.2 Best Local Similarity 42.9 Matches 9; Conservative

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Best Local Similarity 42.9
Matches 9; Conservative
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C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 11-Apr-1997
C;Accession: A34080
E;Ohmachi, T.; Giorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostellum discoideum ub
A;Reference number: A34080; MUID:89352609
A;Accession: A34080
A;Accession: A34080
A;Accession: A34080
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-532 cOHM>
A;Experimental source: strain B, clone DCUB14
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K;Glorda, R.; Ennis, H.L.
Mol. Cell. Biol. 7, 2097-2103, 1987
A;Title: Structure of two developmentally regulated Dictyostellum discoideum ubiquitin A;Reference number: A27806; MUID:87257921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyubiquitin 5 (clone pLK229) - slime mold (Dictyostellum discoideum)
C;Species: Dictyostellum discoideum
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
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A; Residues: 1-381 <G10>
A; Residues: 1-381 <G10>
A; Cross-references: EMBL.M19491; NID:g167950; PIDN:AAA33269.1; PID:g167951
A; Experimental source: strain B, clone pLK229
C; Superfamily: polyubiquitin B, ubiquitin homology
C; Keywords: nucleus; polyprotein; protein degradation
F; 1-76/Product: ubiquitin #status predicted <UB1>
F; 77-152/Product: ubiquitin homology <UBH1>
F; 77-152/Product: ubiquitin homology <UBH2>
F; 77-152/Pomain: ubiquitin homology <UBH2>
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                                                 F;153-228/Froduct: ubiquitin #status predicted <UB3>
F;153-228/Domain: ubiquitin homology <UBH3>
F;259-304/Pormain: ubiquitin #status predicted <UB4>
F;229-304/Domain: ubiquitin homology <UBH4>
F;305-380/Product: ubiquitin #status predicted <UB5>
F;305-380/Domain: ubiquitin homology <UBH5>
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F;77-152/Product: ubiquitin #status predicted <UB2>
                          77-152/Domain: ubiquitin homology
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10 GKTITLEVEGSDNIENVKAKI 30
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Best Local Similarity
Matches 9; Conserv
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N;Alternate names: cytotactin; hexabrachion
N;Contains: tenascin 190K; tenascin 200K
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A32230; B32230; A33379; B33379; C33379; S01292; A30903
R;Jones, F.S.; Hoffman, S.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1999, 1989
A;Title: A detailed structural model of cytotactin: protein homologies, alternative R
A;Reference number: A32230; MUID:89184536
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A.Molecule type: mRNA
Residues: 1-1044,1318-1810 <-JO2>
A.Cross-references: GB:J04519
R.Spring, J.; Beck, K.; Chiquet-Ehrismann, R.
Cell 59, 325-334, 1989
A.Title: Two contrary functions of tenascin: dissection of the active sites by recomb
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A; Residues: 1-204, 'G', 206-221, 'A', 223-380, 'D', 382-386, 'H', 388-444, 'HN', 447-450, 'V', 45
A; Cross-references: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
A; Accession: B33379
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A;Accession: C33379
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R;Pearson, C.A.; Pearson, D.; Shibahara, S.; Hofsteenge, J.; Chiquet-Ehrismann,
EMBO J. 7, 2977-2982, 1988
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A; Residues: 1-1810 <JON>
A; Cross-references: GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
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                                                                                                                                                Fig. 7-152/Product: ubiquitin #status predicted <UB2>
Fig. 7-152/Domain: ubiquitin #status predicted <UB2>
Fig. 7-152/Domain: ubiquitin #status predicted <UB3>
Fig. 7-228/Product: ubiquitin homology <UBH3>
Fig. 229-304/Product: ubiquitin homology <UBH3>
Fig. 209-304/Product: ubiquitin #status predicted <UB4>
Fig. 209-304/Product: ubiquitin homology <UBH4>
Fig. 209-306/Domain: ubiquitin #status predicted <UB5>
Fig. 380-780/Product: ubiquitin homology <UBH5>
Fig. 381-456/Product: ubiquitin #status predicted <UB6>
Fig. 381-456/Domain: ubiquitin homology <UBH6>
Fig. 7-32/Product: ubiquitin #status predicted <UB6>
Fig. 7-32/Product: ubiquitin #status predicted <UB7>
Fig. 7-32/Product: ubiquitin #status predicted <UB7>
Fig. 7-532/Product: ubiquitin homology <UBH7>
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C;Superfamily: polyubiquitin 7; ubiquitin homology C;Keywords: nucleus; polyprotein; protein degradation F;1-76/Product: ubiquitin #status predicted <UBl> F;1-76/Pomain: ubiquitin homology <UBHI>
                                                                                                                                                                                                                                                                                                                           predicted <UB4>
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A; Accession: A33379
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Gaps

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Length 427; Indels

5; DB 7

0; Mismatches Score 42; Pred. No.

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A,Accession: JC5694
A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-427
A,Cross-references: DDBJ:AB001744; NID:g2467307; PIDN:BAA22598.1; PID:d1023466; PID:g
C,Comment: This enzyme is a mitogen-activated protein kinase, and plays a role in egg
C,Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C,Reywords: phosphotransferase
F;24-278/Domain: protein kinase homology <KIN>
                                                                        A)Reference number: JC5693; MUID:97456373
             R;Hashimoto, H.; Matsuo, Y.; Yokoyama, Y.; Toyohara, H.; Sakaguchi, J. Biochem. 122, 381-386, 1997
A;Title: Structure and expression of carp mitogen-activated protein
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
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                                                  Residues: 27-181, R', 183-204, G', 206-221, A', 223-380, D', 382-386, H', 388-444, HN', 447-670-82 references: EMBL: X08030
Gross-references: EMBL: X08030
Superfamily: tenascin; BGF homology; fibrinogen beta/gamma homology; fibronectin type Reywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell 1-122/Domain: signal sequence #status predicted <SIG>
31-32/Domain: propeptide #status predicted <PRO>
34-1810/Product: tenascin 230K #status predicted <AMT>
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A; Molecule type: mRNA
A; Residues: 27-181, 'R',183-204,'G',206-221,'A',223-380,'D',382-386,'A',Coss-references: EMBL:X08030
A; Cross-references: EMBL:X08030
A; Note: part of this sequence was confirmed by protein sequencing C; Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homolog C; Keywords: alternative splicing; calcium binding; cell adhesion; du F; 1-22/Domain: signal sequence #status predicted <PRO>F; 23-34/Domain: propeptide #status predicted <PRO>F; 34-1810/Product: tenascin 330 # status predicted <PRO>F; 34-1810/Promain: EGF homology <EGF>F; 34-1810/Promain: EGF homology <EGF>F; 316-343/Domain: fibronectin type III repeat homology <FN3D>F; 681-765/Domain: fibronectin type III repeat homology <FN3D>F; 773-857/Domain: fibronectin type III repeat homology <FN3D>F; 865-949/Domain: fibronectin type III repeat homology <FN3D>F; 1046-1128/Domain: fibronectin type III repeat homology <FN3D>F; 1046-1128/Domain: fibronectin type III repeat homology <FN3D>F; 1137-1219/Domain: fibronectin type III repeat homology <FN3D>F; 1287-1399/Domain: fibronectin type III repeat homology <FN3D>F; 138-1399/Domain: fibronectin type III repeat homology <FN3D>F; 138-1399/Domain: fibronectin type III repeat homology <FN3D>F; 1495-1575/Domain: fibronectin type III re
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Pred. No. 1.8e+02;
2; Mismatches 3; Indels
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Best Local Similarity 58.3
Matches 7; Conservative
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STRAIN=ISOLATE P307;
MEDLINE=ISOLATE P307;
Dallas W.S., Falkow S.;
"Amino acid sequence homology between cholera toxin and Escherichia coli heat-labile toxin.";
Nature 288:499-501(1980).
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ISOLATE P307;
MEDLINE=85156481; PubMed=3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit c1strons from Escherichia coli of human and porcine origin.";
Infect. Immun. 48:73-77(1985).
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STRAIN=ISOLATE PCG86;
MEDLINE=81137303; Pubmed=3546273;
Yamamento T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae 01.";
J. Bacteriol. 169:1352-1357(1987).
                                                                                                                                                                                            P32890; P13768; P01557;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B, PORCINE) (LTP-B).
ELTB OR LTPB.
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                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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                   SR54_THEAC
IL/R_MOUSE
CD5_RAT
INR1_SHEEP
BCHD_CHLVI
HS7C_CAEEL
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DPOL_HPBVM
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MEDLINE-93240541; PubMed-8478941;
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MEDLINE-91238966; PubMed-2034287;
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MEDILINE-9325225; PubMed-8486242;
Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.;
"Amino acid sequence of heat-labile enterotoxin from chicken
enterotoxigenic Escherichia coli is identical to that of human strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ISOLARE H10407;
MEDLINE-831146.81; PubMed-6759877;
Yamamoto T., Tamura T.A., Yokota T., Takano T.;
"Overlapping genes in the hear-labile enterotoxin operon originating from Escherichia coli human strain.";
Mol. Gen. Genet. 188:356-359(1982).
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"Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coli of human and porcine origin.";
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                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B, HUMAN) (LTH-B).
                                                                                                                                                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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"Identification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins. of Bscherichia coli and Vibrio cholerae.";
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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J. Biol. Chem. 274:8764-8769(1999)
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M.,
Witholt B., Hol W.G.J.;
"Crystal structure of a cholera toxin-related heat-labile enterotoxin
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-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
J. Biol. Chem. 274:8764-8769(1999).
-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED
-!- THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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Gaps

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Length 124; Indels

100.0%; Score 107; DB 1; 100.0%; Pred. No. 3.2e-10; Live 0; Mismatches 0;

Conservative

Best Local Similarity Matches 21; Conserv

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Query Match

GETFOVEVPGSQHIDSQKKAI 86 GETFQVEVPGSQHIDSQKKAI 21

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SEQUENCE.

us-09-786-648-5.rsp

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cholerae
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STRAIN-EL TOR 2125;
MEDLINE-84068199; PubMed-6646234;
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
Honda T.;
                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                Lockman H., Kaper J.B.; "Nucleotide sequence analysis of the A2 and B subunits of Vibrio cholerae enterotoxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cholera toxin genes: nucleotide sequence, deletion analysis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lebens M., Holmgren J., \mbox{\ensuremath{\tt \$Structure}} and arrangement of the cholera toxin genes in Vibrio
                                                                                                                                                                           ;
                                                                                  HEAT-LABILE ENTEROTOXIN B CHAIN.
                                                                                                                                                        94.4%; Score 101; DB 1; Length 124; 95.2%; Pred. No. 2.9e-09; Live 0; Mismatches 1; Indels
                                                                                                            H10407).
H10407).
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-EL TOR 2125;
Dams E., de Wolf M., Dierick W.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
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H -> Y (IN ISOLATE H
H -> R (IN ISOLATE H
V; E9F7F7C7B9D3BC47 C
                                                                                                                                                                                                                                                                    P01556; Q91002;
21-JUJ-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
CHOLERA ENTEROTOXIN, BETA CHAIN PRECURSOR.
CTXB OR TOXB OR VC1456.
                                                                                                                                                                                                                                                             124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholerae 0139.";
FEMS Microbiol. Lett. 117:197-202(1994).
                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 258:13722-13726(1983)
                                                                                                                                                                                                                                                             PRT;
EMBL; J01646; AAB02982.1; -.
EMBL; S60731; AAC60441.1; -.
EMBL; X83966; CAA58800.1; -.
PDB; ILTR; 23-MAR-99.
InterPro; IPR001885; -.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
                                                               Enterotoxin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=84061784; PubMed=6315707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-4260B / SEROTYPE 0139;
MEDLINE-94237453; PubMed-8181723;
                                                                                                                              14027 MW;
                                                                                                                                                                                              1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                       66 GATFQVEVPGSQHIDSQKKAI 86
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STRAIN~1854 / O139-BENGAL;
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine development.";
Nature 306:551-557(1983).
                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                  Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                            Vibrio cholerae.
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                                                                         SIGNAL
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STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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MEDLINE=95387394; PubMed=7658472;
Zhang R.G., Westbrook M.L., Westbrook E.M., Scott D.L., Otwinowski Z.,
Maulik P.R., Reed R.A., Shipley G.G.;
"The 2.4 A crystal structure of cholera toxin B subunit pentamer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING TO CELL MEMBRANES.
-- SUBDINI: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN (FROW THE SAME PRECURSOR MOLECULE). LINKED BY AN INTERCHAIN DISULFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Determination of the primary structure of cholera toxin B subunit."; J. Biol. Chem. 252:7249-7256(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merritt E.A., Sarfaty S., van den Akker F., L'Hoir C., Martial J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crystal structure of cholera toxin B-pentamer bound to receptor GM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TARAIN CRYSTALLOGRAPHY (2.0 ANGSTROMS).
STRAIN-OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE-97376625; PubMed-9232653;
MERLITE E.A., Sarfaty S., Jobling M.G., Chang T., Holmes R.K.,
Hirst T.R., Hol W.G.J.;
"Structural studies of receptor binding by cholera toxin mutants.";
"Structural studies of receptor binding by cholera toxin mutants.";
"Structural Sci. 6.1516-1528 (1997).
-1- FUNCTION: THE BETA CHAIN AGGREGATE (B SUBUNIT) IS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                            "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-78005537; Pubmed-903363;
Kurosky A., Markel D.E., Peterson J.W.;
"Covalent structure of the beta chain of cholera enterotoxin.";
J. Biol. Chem. 252:7257-7264(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-94272319; PubMed-8003954;
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Protein Sci. 3:166-175(1994).
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EMBL; X76391; CAA53976.1; --
EMBL; AE004224; AAF94613.1;
PIR; A01819; XVVCB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000).
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1198 ETFONNVPNYOHIGMKR 121
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Matches 9; Conservative
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2733 AA;
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PIR; S15760; S15760
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P49538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine coronavirus MHV (strain A59).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                                                                                                                                       CHOLERA ENTEROTOXIN, BETA CHAIN.
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WEF. 8).
WEF. 2).
WEF. 7 AND 8).
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01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B)
                                                                                                                                                                                                                                                                                                                           Membrane; Enterotoxin; Signal; 3D-structure.
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3CHB; 12-AUG-98.
1CHP; 08-MAR-96.
1CHO; 08-MAR-96.
1FGB; 23-DEC-96.
1FGB; 01-APR-97.
1XTC: 01-AUG-96.
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                     S14624;
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ID RRPB_CVMA5
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Nucleic Acids Res. 18:1825-1832(1990).

-!- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS

A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY
FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
SUBGENOMIC MENAS AND PROGENY VIRION RNA.

-!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
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Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;

"The chloroplast genome of a chlorophyll a+c-containing alga,
Odontella sinensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Odontella sinensis."; .
Plant Mol. Biol. Rep. 13:336-342(1995).
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE TATC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA-directed RNA polymerase; Helicase; ATP-binding 22 824 POLYMERASE.
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Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBI_TaxID=2839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                              -!- MISCELLANEOUS: THIS PROTEIN MAY BE TRANSLATED AS A 1A-1B POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING MECHANISM.
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Pred. No. 66;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 CYS/HIS-RICH.
06 HELICASE.
27 ATP (BY SIMILARITY).
309218 MW; F3ACCREF20D20C41 CRC64;
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Last annotation update)
PROTEIN YCF43 (ORF263).
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01-FEB-1996 (Rel. 33, Last seq
01-COT-2000 (Rel. 40, Last seq
HYPOTHETICAL 30.1 KDA PROTEIN IN
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52.9%;
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Transferase:
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UBIQUITIN.
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P08618;
                                            RRPB_CVMJH
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SEQUENCE
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                         RESULT 7
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UBIQ_DICDI
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                                                                                                                                                         Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                  Grossman A., Mittrucker H.W., Antonio L., Ozato K., Mak T.W.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 1; Length 467;
Pred. No. 14;
6; Mismatches 4; Indels
                                                                                                                                      Length 263;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; DNA-binding; Nuclear protein. DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT. SEQUENCE 467 AA; 53129 WW; 7E28F5E0F5BA4053 CRC64;
                                                                                                        30080 MW; 25083364F2A89E88 CRC64;
                           Transmembrane
                                                                                                                                      1;
                                                                                                                                                                                                                                                                                        update)
                                                                                                                                     Score 44; DB
Pred. No. 7.8;
                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update
                                                                                                                                                         Mismatches
                       Hypothetical protein, Transm 53 73 POTENTIAL. 103 123 POTENTIAL. 150 POTENTIAL. 151 173 173 POTENTIAL. 181 201 POTENTIAL. 213 233 POTENTIAL.
                                                                                                                                                                                                                                                                                                  INTERFERON REGULATORY FACTOR 6 (IRF-6).
                                                                                               POTENTIAL
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15-JUL-1998 (Rel. 36, Last seq
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF027292; AAB84111.1; -. EMBL; AL022398; CAA18545.1; -. HSSP; P23906; 11RG.
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PROSITE; PS00601; IRF; 1.
                                                                                                                                     41.1%;
40.0%;
                                                                                                                                                                                        41.18;
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Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                  STANDARD;
                PROSITE; PS01218; TATC;
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                                                                                                                           Ouery Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                       (Human)
                                                                                    213
241
263 AA;
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                         Chloroplast;
TRANSMEM
                                                                                                                                                                                                                                                                                                                       Homo sapiens
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014896;
                                           TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA, SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDIATE PLANCE 1846489;
MEDIATE-9111976; PubMed=1846489;
Lee H.-J., Shieh C.-K. Gorbalenya A.E., Koonin E.V., la Monica N., Tuler J., Bagdzhardzhyan A., Lai M.M.C.;
"The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the putative proteases and RNA polymerase.";
virology 180:567-582(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY
                                                                                                                                                                  Murine coronavirus MHV (strain JHM).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA-directed RNA polymerase; Helicase; ATP-binding.
522 824 POLYMERASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: THIS PROTEIN MAY BE TRANSLATED AS A 1A-1B POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING MECHANISM.
-!- SIMILARITY: TO THE AVIAN CORONAVIRUS IBV RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 2731;
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W; 73B3C4025244CEE5 CRC64;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                    01-APR-1993 (Rel. 25, Created)
1-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B).
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2731 AA
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HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44;
Pred. No.
PRT;
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MEDLINE-88152253; PubMed=2831095;
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hes 9; Conservative
STANDARD;
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01-AUG-1988 (Rel. 08,
01-NOV-1991 (Rel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ETFQVEVPGSQHI 14
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fibrinogen.";
                                                                   SEQUENCE
                       BINDING
                                               VARIANT
                                                                                                                                                                                                                                                                                                                                            RESULT 9
TENA_CHICK
                                                                                                                                                                                 Matches
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or send an email to license@isb-sib.ch).
                                      "Complete cDNA sequence of a Dictyostellum ubiquitin with a carboxy-terminal tail and identification of the protein using an anti-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Westphal M., Mueller-Taubenberg A., Noegel A., Gerisch G.;
"Transcript regulation and carboxyterminal extension of ubiquitin in Dictyosteltum discoldeum.";
FEBS Lett. 209:92-96(1986).
-!- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                       MEDLINE-87257921; PubMed-3037345; Giorda R., Ennis H.L.; "Structure of two developmentally regulated Dictyostellum discoideum ubiquitin genes."; MAI. Cell. Biol. 7:2097-2103(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: UBIQUITIN IS SYMTHESIZED AS A POLYUBIQUITIN PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
                                                                                                                                                                                                 Obmachi T., Glorda R., Shaw D.R., Ennis H.L.;
Molecular organization of developmentally regulated Dictyostelium
discoideum ubiquitin CDMss.";
Blochemistry 28:5226-5231(1989).
Mueller-Taubenberger A., Westphal M., Jaeger E., Noegel A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NECESSARY FOR BRANCHED-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X07210; CAA30183.1; ALT_TERM. EMBL; M19666; AAA33261.1; ALT_TERM. EMBL; M19492; AAA33261.1; ALT_TERM. EMBL; M23748; AAA33262.1; ALT_TERM. EMBL; M23749; AAA33262.1; ALT_TERM. EMBL; M23750; AAA33262.1; ALT_TERM. EMBL; M23751; AAA33265.1; ALT_TERM. EMBL; M23751; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM. EMBL; M24762; CAA28408.1; ALT_TERM.
                                                                                                                                                                              MEDLINE-89352609; PubMed-2548604;
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PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
Nuclear protein; Polyprotein.
SITE
                                                                                                         FEBS Lett. 229:273-278(1988).
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InterPro; IPR000626; -.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 13-76 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, A27806; A27806.
PIR, B27806; B27806.
PIR, A34080; A34080.
PIR, B34080; B34080.
PIR; C34080; C34080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UQDOR7
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                                                                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02248;
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PIR; E34080;
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RATE TO THE PROPERTY OF THE PR
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-!- FUNCTION: SAM (SUBSTRATE-ADHESTON MOLECULE) THAT APPEARS TO INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROWTH OF EPTTHELIAL TUMORS.
-!- SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COLLED-COLIL RESTON AND MAY BE STABILIZED BY DISULFIDE RINGS AT BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIDE LINKED WITHIN THE CENTRAL GLOBULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 464-1018 AND 1412-1661 FROM N.A., AND SEQUENCE OF 852-868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -: SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-: ALTERNATIVE PRODUCTS: 3 ISOFORNS: 230 KDA (SHOWN HERE), 200 KDA AND 190 KDA, ARE PRODUCTS: BY ALTERNATIVE SPLICING. THEY ARE PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPMENT.
-: INDUCTION: BY TGF-BETA.
-: SIMILARITY: CONTAINS 13.5 EGF-LIKE DOMAINS.
-: SIMILARITY: CONTAINS 11.5 EGF-LIKE DOMAINS.
-: SIMILARITY: CONTAINS 11.5 FIBRONECTIN TYPE III-LIKE DOMAINS.
-: SIMILARITY: CONTAINS 12.5 EGF-LIKE TO THE C-TERMINAL PART OF THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Embryo;
MEDLINE-88176910; PubMed-2451243;
Jones F.S., Burgoon M.P., Hoffman.S., Crossin K.L., Cunningham B.A.,
Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A cDNA clone for cytotactin contains sequences similar to epidermal growth factor-like repeats and segments of fibronectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TENA_CHICK STANDARD; PRT; 1808 AA.
P10039; P1132; 073584; 073585;
01-MAR-1999 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-CCT-2000 (Rel. 40, Last sequence update)
TENARSCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN)
(GMEM) (J1) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spring J., Beck K., Chiquet Ehrismann R.; "Two contrary functions of tenascin: dissection of the active sites by recombinant tenascin fragments.";
                                                                                                                                                                                                                                                            ö
MULTIUBIQUITIN ADDUCTS.
COUNDGATION TO ACCEPTOR PROTEINS.
K -> N (IN SOME CLONES REPEATS).
6427383968EA8A84 CRC64;
                                                                                                                                                                                          1; Length 76
                                                                                                                                                                                                                                                            7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-722 FROM N.A., AND SEQUENCE OF 79-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fibroblast;

MEDLINE-89030589; PubMed-2460335;
PETSOC C.A., Pearson D., Shibahara S., Hofsteenge Chiquet-Ehrismann R.;
                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                             Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90030407; PubMed-2478295;
                                                                                                                                                                                                                                                                                                                                                                21
                                 76
11
8538 MW;
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                                                                                                                                                                                                                                                            9; Conservative
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                                                                                                                                                                                             Query Match
Best Local Similarity
                                 76
11
76 AA;
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01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
SUPRESSOR OF TUMORIGENICITY 14 (EC 3.4.21.-) (MATRIPTASE) (MEMBRANE-TYPE SERINE PROTEASE 1) (MT-SP1).
ST14 OR PRSS14 OR SNC19.
BY SIMILARITY.
BY SIM
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58.3%; Pred. No. 88;
ive 2; Mismatches 3; Indels
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les 7; Conserv
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Q9Y5Y6;
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ST14_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PF00008; EGF; 13.
Pfam; PF000147; fibrinogen_C; 1.
Pfam; PF000141; fibrinogen_C; 1.
PROSITE; PS00022; EGF_1; 14.
PROSITE; PS01186; EGF_2; 14.
Glycoprotein; Cell adhesion; Repeat; EGF-like domain; Coiled coil; Extracellular matrix; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLED COIL (POTENTIAL).

EGF-LIKE 1 (INCOMPLETE).

EGF-LIKE 3.

EGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.
                                                                                                                                                          EMBL; X08031; CAB40811.1; -...
EMBL; X08030; CAB30824.1; ALT_TERM.
EMBL; X08030; CAB30824.1; ALT_SEQ.
EMBL; M3091641; AAA48749.1; ALT_SEQ.
PIR; A310903; A31093.
PIR; A31930; A31930.
PIR; A31379; A31379.
PIR; B33379; B33379.
PIR; S03292; S03292.
HSSP; P24821; ITEN.
                                                                                                                                             EMBL; M23121; AAA49086.1; -.
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000561; -. InterPro; IPR001777; -. InterPro; IPR002181; -.
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                                                                                         94769
                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                     STANDARD;
 603
851
656
711
805
109
302
485
                                                                                                                                                                            1::|||:||:
367 TWNIEVPNNQHV 378
                                                                                                                                                                 3 TFQVEVPGSQHI 14
                                                                                 772
855 AA;
                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                           ARO2 OR YGL148W.
                                                                                                                                                                                                                                                                                                  PHOSPHOLYASE)
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P28777:
                                                                                                                                                                                                                                                                                                                                                                                                                                 cerevisiae
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CARBOHYD
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-99303581; PubMed-10373424;
Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
"Molecular cloning of cDNA for matriptase, a matrix-degrading serine protease with trypsin-like activity.";
J. Blol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                      SEQUENCE FROM N.A.

Takeuchi T., Shuman M.A., Craik C.S.;

Takeuchi T., Shuman M.A., Craik C.S.;

"Reverse blochemistry: Use of macromolecular protease inhibitors the dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";

Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R InterPro; IPR0001254; -.
R InterPro; IPR001254; -.
R InterPro; IPR001254; -.
R InterPro; IPR001214; -.
R InterPro; IPR001312; -.
R Pfam; PF000657; Id_Lrecept_a; 4.
R Pfam; PF00069; trypsin; 1.
R Pfam; PF00721; Culy.
R PRINTS; PR00761; LDLRECEPTOR.
R PRINTS; PR0014; TRYPSIN.IR; 1.
R PROSITE; PS001180; TRYPSIN.IR; 1.
R PROSITE; PS01180; CUB; 2.
R PROSITE; PS0109; LDLRA_1; 2.
R PROSITE; PS50068; LDLRA_1; 2.
R PROSITE; PS50068; LDLRA_2; 4.
R Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
R Transmembrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUB 1.
CUB 2.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
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334
447
487
524
560
  sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                TRYPSIN FAMILY
                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                PubMed-10373425;
                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: REDUCED FLAVIN.
-!- PATHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
-!- SUBUNIT: HOMOTETRAMER (EY SIMILMARITY).
-!- INDUCTION: BY AMINO ACID STARVATION.
-!- SIMILMARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-BEC-1992 (Rel. 39, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92114793; PubMed-1837329;
Jones D.G.L., Reusser U., Braus G.H.;
"Molecular cloning, characterization and analysis of the regulation
of the ARO2 gene, encoding chorismate synthase, of Saccharomyces
                                                      CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1; Length 855;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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LDL-RECEPTOR CLASS A 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 5:2143-2152(1991)
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genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "4-aminobutyrate aminotransferase (GABA-transaminase) deficiency.";
J. Inherit. Metab. Dis. 22:414-427(1999).
-!- CATALYTIC ACTIVITY: 4-AMINOBUTANOATE + 2-OXOGLUTARATE = SUCCINATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medina-Kauwe L.K., Tobin A.J., De Meirleir L., Jaeken J., Jakobs C.,
Nyhan W.L., Gibson K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Biase D., Barra D., Simmaco M., John R.A., Bossa F.;
"Primary structure and tissue distribution of human 4-aminobutyrate
aminotransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - TISSUE SPECIFICITY: LIVER > PANCREAS > BRAIN > KIDNEY > HEART >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osei Y.D., Churchich J.E.; "Screening and sequence determination of a cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT DEFICIENCY PHENOTYPE INCLUDES PSYCHOMOTOR RETARDATION, HYPOTONIA,
                                                                                                                                                                                                                                        Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHOUDRIAL PRECURSOR (EC 2.6.1.19) (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA AMINOTRANSFERASE) (GABA-AT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPERREFLEXIA, LETHARGY, REFRACTORY SEIZURES, AND EEG
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                      AF3AF65605B91E8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 368-465 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: MONOMER (PROBABLE).
-!- SUBCELLUIAR LOCATION: MITOCHONDRIAL MATRIX.
                                  Pfam; PF01264; Chorismate_synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.
Lyase; Aromatic amino acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 AA
                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                      38.8%; Score 41.5; 62.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4-aminobutyrate aminotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 227:476-480(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99336116; PubMed=10407778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95154329; PubMed=7851425;
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                                                                                                                                                                      40838 MW;
                                                                                                                                                                                                                                    Query Match 38.8
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                      258 GSGFQGVSVPGSKHND 273
                                                                                                                                                                                                                                                                                                                          1 GETFQ-VEVPGSQHID 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 155:185-187(1995).
S17246; S17246
S0003116; ARO2
                                                                                                                                                                        376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GABT_HUMAN
                                                                                                                                                                      SEQUENCE
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GABT_HUMAN
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or send an email to license@lsb-sib.ch).
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"Peptidase D gene (pepD) of Escherichia coli K-12: nucleotide
sequence, transcript mapping, and comparison with other peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T., Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S., Mizuno T., Makino K., Nakata A., Yura T., Sampei G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                    4-AMINOBUTYRATE AMINOTRANSFERASE.
PYRIDOXAL PHOSPHATE.
R -> K (IN GABA-AT DEFICIENCY; 25%
REDUCTION IN ACTIVITY).
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                                                                                                                                                                                                                                 Pfam; PF00202; aminotran_3; 1.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
Transferase; Aminotransferase; Pyridoxal phosphate;
Neurotransmitter degradation; Mitochondrion; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 500;
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D -> H (IN REF. 2).

V -> L (IN REF. 2).

E -> G (IN REF. 2).

K -> Q (IN REF. 2).

W -> G (IN REF. 2).

S -> A (IN REF. 2).

G -> R (IN REF. 2).

G -> R (IN REF. 2).

C -> G (IN REF. 2).

C -> G (IN REF. 2).

L -> H (IN REF. 2).

W, 41199085693F80AD CRC64;
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ë,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFH_ECOLI STANDARD; PRT; 141 AA. P28369; P77246; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) PEPTIDE CHAIN RELEASE FACTOR HOMOLOG (RF-H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.5; DE
Pred. No. 39;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90330577; PubMed-1695895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 172:4641-4651(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.8%;
55.6%;
                                                                                                                                                                 EMBL; L32961; AAA74449.1; -.
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17 TYRLLVPGSRHI-SQAAA 33
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                                                                                                                                                                                                              InterPro; IPR000954; -.
                                                                                                                                                                                                                                                                                                                                                 28
500
357
220
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132
191
204
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STRAIN-K12 / W3110;
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A);
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                                                                                                                                                                                                                                                                                                                              Disease mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
1113
1132
1204
2206
320
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29
357
220
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VARIANT
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Romier C., Reuter K., Suck D., Fiener R.;
Crystal structure of tRNA-guanine transglycosylase: RNA modification
by base exchange.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shark K.B., Conway T.; "Cloning and molecular characterization of the DNA ligase gene (lig) from Zymomonas mobilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graedler U., Gerber H.D., Goodencough Lashua D.M., Garcia G.A.G., Ficner R., Reuter K., Stubbs M.T., Klebe G.; "A new target for shigellosis: rational design and crystallographic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reuter K.K.H., Ficner R.; "Sequence analysis and overexpression of the Zymomonas mobilis tgt "Sequence analysis and overexpression of the Zymomonas mobilis tgt blochemical characterization of the enzyme."; J. Bacteriol. 177:5284-5288(1995).
                                                                                                                    Submitted (FEB-1995) to the EWBL/GenBank/DDBJ databases.
-! SIMILARITY: SOME, TO YEAST YDLO87C AND S.POMBE SPCCIGAll.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGT_ZYMMO STANDARD; PRT; 385 AA.
P28720; Q60247;
01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OUGUINE TRNA-RIBOSYLITRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.3%; Score 41; DB 1; Length 313; 46.2%; Pred. No. 28; Live 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., SEQUENCE OF 1-6, AND CHARACTERIZATION MEDLINE=95394847; PubMed=7665516;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; U21317; AAA62527.1; -.
WormDep; B0495.8; CE01766.
Hypothetical protein. SEQUENCE 313 AA; 36977 MW; 000D2327621BFEDO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Zymomonas mobilis.";
FEMS Microbiol. Lett. 75:19-26(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
STRAIN-ATCC 31821 / ZM4 / CP4;
MEDLINE-92406015; Pubmed-1526462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 15:2850-2857(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EVPGSQHIDSQKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 QLMGSQHVDNKEK 23
                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2:
  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=542;
                                                                                                   Kirsten J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGT_ZYMMO
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or send an email to license@isb-sib.ch).
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MGIRRK -> MLETETGRYSDTLRSALVSLDGDNAWALSES
MGIRRE. 3 AND 4).
9D2EBD9AF7A04831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    [5]

NEDLINE-93027135; PubMed-1408743;

Pel H.J., Rep M., Grivell L.A.;

Sequence comparison of new protaryotic and mitochondrial members of the polypeptide chain release factor family predicts a five-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1 - SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
SEQUENCE FROM N.A.
STARAIN-KIZ / MGIG55;
MEDIJINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rlay M., Collado-Yides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. 20:4423-4428(1992).
COULD BE PROTEIN FACTOR INVOLVED IN TRANSLATIONAL
                                                                                                                                                                                                                                             Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O. Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Length 141;
                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 37.0 KDA PROTEIN B0495.8 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.3%; Score 41; DB 35.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 12;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M34034; -; NOT_ANNOTATED_CDS.
EMBL; D83536; BAA77905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00472; RF-1; 1.
PROSITE; PS00745; RF_PROK_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AA; 16177 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U70214; AAB08656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 ETLRSSGPGGQHVNKTDSAV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D83536; BAA77905.1; -. AE000132; AAC73340.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.3'
Best Local Similarity 35.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG11496; prfH.
InterPro; IPR000352; -.
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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TERMINATION.
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Q09217;
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EMBL;

EMBL;

RESULT 14 YP68_CAEEL

OCCUPATION

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Gaps

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Lambda phage group.
NCBI_TaxID=10719;
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P08979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
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                                                         DEAZAGUANINE IN TRNAS WITH GU(N) ANTICODONS (TRNA-ASP, -ASN, -HIS AD-TYR). AFTER THIS EXCHANGE, A CYCLOPENTENDIOL MOIETY IS ATTACHED TO THE 7-AMINOMETHYL GROUP OF 7-DEAZAGUANINE, RESULTING IN THE HYPERMODIFIED NUCLEOSIDE QUEUOSINE (Q) (7-(((4,5-CIS-DITYDROXY-2-CYCLOPENTEN-1-Y1)AMINO)METHYL) 7-DEAZAGUANOSINE). CATALXITIC ACTIVITY: TRNA GUANINE + QUEUINE = TRNA QUEUINE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                       -1- SUBUNIT: MONOMER.
-1- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMII
-1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY DUE
studies of inhibitors of tRNA-guanine transglycosylase."; Submitted (MAR-2000) to the PDB data bank.
                                                                                                                                                                                                  COFACTOR: BINDS AND REQUIRES ZINC FOR ACTIVITY. ALSO REQUIRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 43.8 KDA PROYEIN IN XPAC-ABRB INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tRNA processing; Zinc; Magnesium; 3D-structure.

trna processing; Zinc; Magnesium; 3D-structure.

trna 0 0 0

trna SITE 102 102

CT_SITE 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L3377; AAA27704.1; ALT_INIT.
EMBL; L3377; AAA27705.1; ALT_INIT.
EMBL; Z11910; -; NOT_ANNOTATED_CDS.
PDB; 1PUD; 07-JUL-97.
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ZINC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42738 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-97.
19-APR-00.
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Pfam; PF01702; TGT; 1.
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Best Local Similarity
'-hag 8; Conserve
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                                                                                                                                                                                                                                                                                                   TO FRAMESHIFTS.
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                                                                                                                                                                                                                    MAGNESIUM
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ACT_SITE
METAL
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    SOUTH THE TEST TO 
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MEDLINE-94374705; PubMed=8088546;
Harilay N.M., Murphy G.O., Bruton C.J., Chater K.F.;
"Sequence of the essential early region of phi C31, a temperate phage of Streptomyces spp. with unusual features in its lytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The repressor gene (c) of the Streptomyces temperate phage phi c31: nucleotide sequence, analysis and functional cloning."; Mol. Gen. Genet. 213:269-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.3%; Score 41; DB 1; Length 386; 31.2%; Pred. No. 35; ive 8; Mismatches 3; Indels
                                                                                                                                                                                                                Bookstein C., Edwards C.W., Hulett F.M.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E -> M (IN REF. 2).
D921F3A0F6845EEE CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
REPRESSOR PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 683 AA.
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MEDLINE=89039715; PubMed=3185504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 AA; 43830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D26185; BAA05262.1; -. EMBL; M96156; AAA22892.1; -.
                                                                                                                                                                                      SEQUENCE OF 1-191 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 299104; CAB11802.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sinclair R.B., Bibb M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SubtiList; BG10090; yaan
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Matches 5; Conservative
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                                                                                                                   Res. 1:1-14(1994).
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Gaps

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Length 1702;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
NCBL_TaxID=86030;
                                                                                                                                          DNA POLYMERASE, 1ST PART.
PI-TLI II ENDONUCLEASE (TLI POL-1 INTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 204:153-158(1997).
--- CATALYTIC ACTIVITY. N DEOXYNUCLEOSIDE TRIPHOSPHATE --
N PYROPHOSPHATE + DNN(N).
--- PTM: THIS PROPEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION
(INTEINS) FOLLOWED BY PEFTIDE LIGATION.
--- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                          DNA POLYMERASE, 2ND PART.
PI-TLI I ENDONUCLEASE (TLI POL-2 INTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYMERASE, 1ST PART (POTENTIAL)
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INTEIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR002064: -..
InterPro: IPR002203: -.
Pfam. PF00136; DNA_POL_B; 4.
PRINTS: PR00379; INTERN.
PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
PROSITE; PS00181; PROTEIN_SPLICING; 3.
Transferase: DNA_directed DNA polymerase; DNA replication; DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
                           PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
PROSITE; PS00881; PROTEIN_SPLICING; 2.
Transferase; DNA-directed MA polymerase; DNA replication;
DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Niehaus F., Frey B., Antranikian G., "Cloning and characterisation of a thermostable alpha-DNA from the hyperthermophilic archaeon Thermococcus sp. TY."; Gene 204:153-158(1997).
                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 1, C. Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                             DNA POLYMERASE, 3RD PART. W; 21D6B98C75F53B20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1829 AA
                                                                                                                                                                                                                                                      (IVPS2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98094267; PubMed-9434178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (strain TY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y13030; CAA73475.1; -.
                                                                                                                                                                                                                                                                           1472 1702
1702 AA; 197293
                                                                                                                                                                                                                                                                                                                                                                38.3%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 46...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 GDSFAVEIKGRIHFD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
         PRINTS; PR00379; INTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHID 15
                                                                                                                                          494
1032
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1471
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769
855
1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                       Protein splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein splicing
                                                                                                                                                 1
495
                                                                                                                                                                                                          1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPOL_THEST
033845;
                                                                                                                                                                                                                                                                             CHAIN
SEQUENCE
                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
N PYROPHOSPHATE + DNA (N).
N PYROPHOSPHATE + DNA (N).
PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
A POST-TRANSLATIONAL EXCISION OF THE TWO INTERVENING REGION
(INTEINS) FOLLOWED BY PEPTIDE LIGATION.
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermococcus litoralis.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus
NCBI_TaxID=2265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
-i- FUNCTION: INTEIN ENCODED ENDONUCLEASES ARE THOUGHT TO MEDIATE
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTEIN MOBILITY BY SITE-SPECFIC RECOMBINATION INITIATED BY ENDONUCLEASE CLEAVAGE AT THE "HOMING SITE" IN GENE THAT LACK THE
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DNA POLYMERASE (EC 2.7.77) (VENT DNA POLYMERASE) (CONTAINS: PI-TLI ENDONUCLEASE; PI-TLI II ENDONUCLEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDIINE-92302285; PubMed-1608969;
Perler F.B., Comb D.G., Jack W.E., Moran L.S., Qiang B.,
Kucera R.B., Benner J., Slatko B.E., Nwankwo D.O., Hempstead S.K.,
Carlow C.K.S., Jannasch H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SPLICING.
MEDILIES-93117083; PubMed-1475179;
HOdges R.A., Perler F.B., Noren C.J., Jack W.E.;
"Protein splicing removes intervening sequences in archaea DNA
                                                                                                                                                                                                          ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Intervening sequences in an Archaea DNA polymerase gene.";
Proc. Natl. Acad. Sci. U.S.A. 89:5577-5581(1992).
                                                                                                                                                            38.3%; Score 41; DB 1; Length 683; 50.0%; Pred. No. 65; ive 2; Mismatches 5; Indels
EMBL; X12865; CAA331345.1; -.
EMBL; X76288; CAA53911.1; -.
PIN; S01433; S01433.
Transcribtion regulation; Repressor; DNA-binding.
SEQUENCE 683 AA; 74077 MW; B02379D204F37D1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1702 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 20:6153-6157(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M74198; AAA72100.1; -. EMBL; M74198; AAA72101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00136; DNA_pol_B; 3.
                                                                                                                                                                                   Best_Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S42459; S42459.
REBASE; 2613; PI-T111.
REBASE; 2621; PI-T1111.
                                                                                                                                                                                                                                                   1 GETFQVEVPGSQHI 14
                                                                                                                                                                                                                                                                                             86 GRIFDIELIGADHI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002064; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002203;
                                                                                                                                                                                                                                                                                                                                                                                                       DPOL_THELI
P30317;
                                                                                                                                                              Query Match
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a IIII

polymerase

B60A605222CBBCAC CRC64;

95797 MW;

862 AA;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
POLYMERASE, 3RD PART (POTENTIAL).
             INTEIN III.
DNA POLYMERASE, 4TH PART (POTENTIAL).
W; All3A8BC57EB9CB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

ISSUE-Badometrial tumor;

MEDLINE-9435239; Pubmed-8072530;

Nicolaides N.C., Papadopoulos N., Liu B., Wei Y.-F., Carter K.C.,
Ruben S.M., Rosen C.A., Haseltine W.H., Fleischmann R.D.,
Fraser C.M., Adams M.D., Venter J.C., Dunlop M.G., Hamilton S.R.,
Petersen G.M., de la Chapelle A., Vogelstein B., Kinzler K.W.;

"Mutations of two PMS homologues in hereditary nonpolyposis colon
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                ö
                                                                                  Length 1829;
                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA repair; Disease mutation; Anti-oncogene; Polymorphism. VARIANT 20 20 R -> Q_{\star}
                                                                                 Score 41; DB 1; Length 182
Pred. No. 1.9e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FIId-VAR_004469.
P -> S (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002099; -.
Pfam; PF01119; DNA_mis_repair; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequ
01-0CT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U14658; AAA50390.1; -. SWISS-2DPAGE; P54278; HUMAN.
                                                                                 38.3%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U13696; AAA63923.1; -.
                                        211875
                                                                                                              Conservative
                                                                                                                                                       STANDARD;
                                                                                                                                       1 GETFQVEVPGSQHID 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer.";
Nature 371:75-80(1994).
1441
                           1829
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                                           ¥.
                                                                                 Query Match
Best Local Similarity
1393
1442
1599
1829
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                        PMS2_HUMAN P54278;
                          CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                             Matches
FFFS
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ST. LAWRENCE 74 / St. 74 / ORS 6A;
MEDLINE-89366647; PubMed-2549509;
Tacciol1 G.E., Grotewold E., Aisemberg G.O., Judewicz N.D.;
"Ubiquitin expression in Neurospora crassa: cloning and sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ST. LAWRENCE 74 / SL 74 / ORS 6A;
MEDLINE-91323720; PubMed-1650731;
Taccioli G.E., Grotewold E., Alsemberg G.O., Judewicz D.N.;
The cDNA sequence and expression of an ubiquitin-tail gene fusion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 147:137-140(1994).
-!- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS. THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANGOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN PRECURSON WITH 4 EXACT HEAD TO TAIL REPEATS. THERE IS A FINAL AMINO-ACID (GLN) AFTER THE LAST REPRAT. SOME UBIQUITIN GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=74-OR23-1A;
MEDLINE=94374698; PubMed=8088539;
Tarawneh K.A., Anumula K.R., Free S.J.;
"The isolation and characterization of a Neurospora crassa gene (ub::crp-6) encoding a ubiquitin-40S ribosomal protein fusion protein.";
                                                    ;
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                  Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
                                                 ö
              Score 40.5; DB 1;
Pred. No. 1e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                              76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a polyubiquitin gene.";
Nucleic Acids Res. 17:6153-6165(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13140; CAA31530.1; ALT_TERM.
EMBL; U01220; AAA56880.1; ALT_TERM.
PIR; S05323; UQNC.
PIRSP; P02248; DAR.
InterPro; IPR000626; -.
                                                   2;
                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
                37.9%;
75.0%;
Query Match
Best Local Similarity 75.v
9; Conservative
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.";
Gene 102:133-137(1991).
                                                                                                       10 GSQ-HIDSQKKA 20
                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 UBIQUITIN.
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UBIQ_NEUCR
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DR DR DR DR DR SS FT FT SS

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PS00014; ER TARGET; 1.
PS00297; HSP70_1; PARTIAL.
PS00329; HSP70_2; PARTIAL.
PS01036; HSP70_3; PARTIAL.
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-89306577; Pubmed-2744444;
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                               :||:|| || : | |
103 DTFEVEKPGGNEEEEQLAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M28528; AAA28076.1; -.
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35.3%;
ETFQVEVPGSQHIDSQKKA 20
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|133 TFEIDVNGILHVSAEDK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TFQVEVPGSQHIDSQKK 19
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                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome 32:190-195(1989)
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InterPro; IPR001023; -.
Pfam; PF00012; HSP70; 1
PROSITE; PS00014; ER_TA
                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T15H9.1.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                  HSP-4 OR HSP70D.
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Q10005;
01-NOV-1997 (
01-NOV-1997 (
                                                                                                                                     RESULT 23
HS74_CAREL
D PS0163; DT 1874_CAREL
D 01-FEB-1991
DT 01-FEB-1991
DT 01-FEB-1991
DT 01-FEB-1991
DT 15-JUL-1998
DE HEAT SHOCK 7
GN Caenorhabdit OC EUKATYOTA; MCC CAENDALITICAL
RN (1)
RN (1)
RN (1)
RN (1)
RA HESCHI M.F. P
RT 11dentificat
CC Rhabditides
CC NCBL_TAXID=69
RN (1)
RN (1)
RP HESCHI M.F. P
RT 11dentificat
CC CAENDAMA
CC This SUNES-P
CC This SUNES-P
CC The EUROPEAN
CC THE SPS1EL
CC THIS SHOWN
CC THE FUTOPEAN
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CC THE FUTOPEAN
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YRY1_CAEEL
N
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: FUNCTIONS BY PROMOTING THE FORMATION OF THE FIRST PEPTIDE BOND (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE BIF-58 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
TRANSLATION INITIATION FACTOR 5A (EIF-5A) (HYPUSINE-CONTAINING
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                  NECESSARY FOR BRANCHED-CHAIN
MULTIUBROUTIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS.
994480FE7D38403E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ko Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Maudua S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.4%; Score 40; DB 1; Length 148; 42.1%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                     37.4%; Score 40; DB 1; Length 76;
42.9%; Pred. No. 9;
Live 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 50 HYPUSINE (BY SIMILARITY).
148 AA; 16205 MW; B7C886047F0FB46F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                       PRINTS; PR00348; UBIQUITIN.
PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP000063; BAA81096.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GKTITLEVESSDTIDNVKQKI 30
                                                                                                           Nuclear protein; Polyprotein.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                    76 AA; 8598 MW;
                                                                                                                                                                                                                                                                                                     Query Match 37.4
Best Local Similarity 42.9
Matches 9; Conservative
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MOD_RES 50 50
SEQUENCE 148 AA; 16
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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Q9YA53;
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                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                        SITE
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HDD BERNAR BERNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY. STRONG,
TO MAMMALIAN GRP78.
                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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PROSITE; PS01036; HSP70_3; PARTIAL.
ATP-binding; Heat shock; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 39.9 KDA PROTEIN 715H9.1 IN CHROMOSOME II PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                       Heschl M.F.P., Baillie D.L.,
"Identification of a heat-shock pseudogene from Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 PREVENT SECRETION FROM ER 31267 MW; 967F5A4A12FA67BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN D (FRAGMENT).
288 AA
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37;
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-!- FUNCTION: NADP+(-)DEPENDENT ADH ACTIVITY.
-!- CATALYTIC ACTIVITY: AN ALCOHOL + NADP(+) - AN ALDEHYDE OR KETONE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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Matches
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
HYPOTHETICAL PROTEIN T15H9.1.
J-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                         Gardner A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95FA4D8E551D9CC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kimura A., Hara Y., Kimoto T., Okuno Y., Minekawa Y.,
Nakabayashi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH3_ENTHI STANDARD; PRT; 395 AA. 024857; 094560; 01-NOV-1997 (Rel. 35, Created) NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) ALCOHOL DEHYDROGENASE 3 (EC 1.1.1.1) (ADH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagn. Lab. Immunol. 3:270-274(1996).
                                                                                                                                                                                                                                                                                                                                                                                                   37.4%; Score 40; DB 47.4%; Pred. No. 47; tive 2; Mismatches
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                                                                                                                                    1- SIMILARITY: CONTAINS 1 J DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-HM-1:IMSS;
MEDLINE-96336080; Pubmed=8705667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HM-1:IMSS;
MEDLINE=96201701; PubMed=8611619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39861 MW;
                                                                                                                                                                                                                                                                                                                                                           EMBL; Z47356; CAA87414.1; -. HSSP; P08622; 1XBL.
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Best Local Similarity
'-has 9; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                    STRAIN-BRISTOL N2;
                                            SEQUENCE FROM N.A.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R -> I (IN REF. 2).
TLENHQDY -> HKKIIKTI (IN REF. 2).
MISSING (IN REF. 2).
WNR -> NE (IN REF. 2).
506FBBA933631FA9 CRC64;
                      FAMILY; MOST SIMILAR TO C.ACETOBUTYLICUM BDHA AND BDHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 1; Length 395;
Pred. No. 52;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF00465; Fe-ADH; 2.
PROSITE; PS00913; ADH_IRON_1; FALSE_NEG
PROSITE; PS00060; ADH_IRON_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 16, 2001, 16:44:05
Job time: 464 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43485 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.4%;
                                                                                                                                                                                                                                                                                          EMBL; D49910; BAA08651.1; -. EMBL; Z48752; CAA88639.1; -. InterPro; IPR001670; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
235
273
273
307
395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Total number of Minimum DB seq Maximum DB seq

Database

Searched:

Perfect score:

Title:

Run on:

Scoring table: Sequence:

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Q9q217 mus musculu
Q9u3m9 caenorhabdi
Q9u16 ovis aries
P97431 mus musculu
Q9p5z5 neurospora
Q9skb2 arabidopsis
Q9nf90 leishmania
Q9nf4 arabidopsis
Q9qmn7 hepatitis b
Q90995 gallus gall
Q90824 gallus gall
Q90824 gallus gall
Q90824 gallus gall
                                                                                                                     042099 cyprinus ca
09hca3 homo sapien
09h3s0 homo sapien
055583 synechocyst
03135 bacilius ce
09epb5 mus musculu
09ey9u6 drosophila
                                                                                                                                                                                      Q9mal6 arabidopsis
O70057 bordetella
                                                                                                                                                                                                               Q9f517 zymomonas m
O04636 arabidopsis
Q9sq79 pinus taeda
                                                                                                                                                                                                      Q43098 psophocarpu
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CLASSICAL STRAIN 569B;
MEDLINE=91355224; PubMed=1883840;
Dams E., De Wolf M., Dierick W.;
"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical strain 569B.";
Blochim. Blophys. Acta 1090:139-141(1991).
                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHOLERA TOXIN B PROTEIN (CTB). D6BF83FFF7924EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu L.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X58785; CAA41591.1; -.
EMBL; U26579; AA34728.1; -.
EMBL; A00931; CAA00098.1; -.
HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA TOXIN B PROTEIN (CTB) PRECURSOR (CTB).
                                                                                                                                                                                                                                                                                                           124 AA
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         Q903M9
Q9N136
P97431
Q9P525
Q9SKB2
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090995
090824
090824
0917A0
094209
094350
091335
091335
090906
097906
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O04636
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Q9SN44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CLASSICAL BIOTYPE 569B;
Shi C., Cao C., Zhang J., Ma Q.;
Chin. Biochem. J. 9:395-399(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001835; -.
Pfam; PF01376; EnterCtoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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124 CH
13919 MW;
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STRAIN=CLASSICAL BIOTYPE 569B;
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124 AA;
   Vibrio cholerae.
   CHAIN
SEQUENCE
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Q57193;
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SIGNAL
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Q57193
   95635 vibrio chol

92prl5 vibrio chol

99987 homo sapien

991jb0 arabidopsis

991gm2 oryza sativ

940742 oryza sativ

999874 arabidopsis

99876 arabidopsis

99876 arabidopsis

99876 arabidopsis

99876 arabidopsis

99978 murine hepa

99136 murine hepa

9938 murine hepa

99938 murine hepa
                                                              July 16, 2001, 16:43:38; Search time 57.41 Seconds (without alignments) 48.396 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                    425026 seqs, 132305027 residues
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107
1 GETFQVEVPGSQHIDSQKKAI 21
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Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
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09SXC9
09P4E0
09LY67
09J3F2
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Q9J3E8
O22511
O49876
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sp_unclassified:*
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sp_mammal:*
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sp_phage:*
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Nezu J., Oku A., Jones M.H., Shimane M.; "Identification of two novel human putative serine/threonine kinases, VRK1 and VRK2, with structural similarity to vaccinia virus BIR
                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95303036; PubMed-7783690;
Nakashima K., Eguchi Y., Nakasone N.;
"Characterization of an enterotoxin produced by Vibrio cholerae
                                                                                      Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.8%; Score 95; DB 2; Length 103; 90.5%; Pred. No. 5.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 45:327-331(1997).
-!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AB000450; Baa19109.1; -.
HSSP; Q06486; 1CKI.
InterPro; IPR000719; -.
                                                                                                                        1; Indels
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Interpro; IPR001835; -.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
SEQUENCE 124 AA; 13905 MW; 23BF83FFF793E5B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ol-mar-1997 (TrEMBLrel. 03, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
                                                                                      Score 101; DB 2;
Pred. No. 7.3e-09;
                                                                                                                                                                                                                                                                                    103 AA
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                                                                                                                                                           1 GETFOVEVPGSQHIDSQKKAI 21
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                                                                                      Query Match 94.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                               66 GATFQVEVPGSQHIDSQKKAI
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Best Local Similarity 90.59
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SEQUENCE FROM N.A.
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                                                                         Gaps
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NCBI_TaxID=666;
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nuclecide sequence analysis of the virulence gene
cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misalimurbag Hoiji 35:205-210(1999).
EMBL; AFI75708; Aab51360.1; -.
HSSP; P01556; 2CHB.
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Yamamoto K., Do V.G., Xu M., Iida T., Miwatani T., Albert M.J.
                                    Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.4%; Score 101; DB 2; Length 124; 95.2%; Pred. No. 7.3e-09; Ive 0; Mismatches 1; Indels
                                                                     1; Indels
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3F87B2F297953179 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA ENTEROTOXIN B-SUBUNIT.
                                  94.4%; Score 101; DB 2;
95.2%; Pred. No. 7.3e-09;
iive 0; Mismatches 1;
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Pfam; PF01376; EnterOtoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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                                                                                                                        66 GATFQVEVPGSQHIDSQKKAI 86
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                                                                     Conservative
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                                                 Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
Matches 20; Conserv
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                                    Query Match
                                                                                                                                                                                                                           Q56635
Q56635;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                       SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryas astiva nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0433F09.";
                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 10; Length 428;
Pred. No. 7.4;
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                Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0041E11.";
                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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"Characterization and expression of a rice RAD23 gene.";
Plant Mol. Biol. 34:557-562(1997).
EMB: U65530, AAB65841.1; --
HSSP; P02248; ITBE.
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                                                                                                                                                                                           Submitted (100-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002521; BAA96762.1; -.
EMBL; AP002539; BAB08201.1; -.
Interpro: IPR001552; -.
Pfam; PF00441; Acyl-CoA_dh; 1.
PROSITE; PS00073; AcYL_COA_DH_2; UNKNOWN_1.
SEQUENCE 428 AA; 46132 MW; 8D34E369BABE6367 CRC64;
                                                                       Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 14;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last anno
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InterPro; IPR000449; -.
InterPro; IPR00626; -.
Fam; PF00240; ubiquitin; 1.
Pfam; PF00627; UBA; 2.
PROSITE; PS50053; UBIQUITIN_2; 1.
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MEDLINE=97369378; PubMed=9225866;
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Best Local Similarity 42.9
Matches 9; Conservative
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         STRAIN-CV. NIPPONBARE;
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Q40742;
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicales; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tabata S.;
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Pred. No. 3.2;
InterPro; IPR002290; -.
PROMITE: PS00101; PROTEIN KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_SI; 1.
SAMRT; SM00220; S_TKC; 1.
ATF-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 508 AA; 58126 MW; 157FBF8F48511AF4 CRC64;
                                                                                                                                                         50.5%; Score 54; DB 4; Length 508, 50.0%; Pred. No. 1.4; 7; Indels iive 3; Mismatches 7; Indels
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Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Ta
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 7:217-221(2000).
EMBL; AP000606; BAB01195.1; -.
SEQUENCE 552 AA; 63036 MW; 740EA16CDEBB2447 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
EMB|CAB7996.1.
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Last annotation update)
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                                                                                                                                                                                                                                                329 GQSINVHTPNSQKVDSQKAA 348
                                                                                                                                                                                                                              1 GETFQVEVPGSQHIDSQKKA 20
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Best Local Similarity 58.8%;
Matches 10; Conservative
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                                                                                                                                                                           Best Local Similarity 50.0
Matches 10; Conservative
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SEQUENCE FROM N.A.
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PubMed=10907853;
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Submitted (APR-1999) to the E
EMBL; AC00657; AAD25769.1; -
INTECPTO; IPRO00665; -
Pfam; PF00240; ubiquitin; 2.
SEQUENCE 91 AA; 10142 MW;
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Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Zieran L.L., Rubin G.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003408; AAF44471.].
                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
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Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Kremenetskala I., Luros J., Ngan i., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huzar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC F1511 sequence.";
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Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Bragnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                  Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A. Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw
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Pred. No. 14;
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395 AA; 43561 MW; AE4F1CC4ADD3DA73 CRC64;
                                         01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
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Last annotation update)
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                          .-OCT-2000 (TrEMBLrel. 15, Created)
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STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed-10471707;
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56.2%;
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Best Local Similarity 56.2
Matches 9; Conservative
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NCBI_TaxID=7227;
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SEQUENCE 3
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09NKD5;
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STRAIN-CV COLUMBIA:
VYSOISKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
VySOISKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
VySOISKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Hizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Arabidopsis thaliana chromosome 1 BAC T17H3 sequence.";
Submitted (AnG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO05916; AAD45990.1;
InterPro; IPR001382;
Primm, PF0132; Glycolhydro_47; 1.
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                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 574;
                                                                          Length 91;
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SEQUENCE 574 AA; 65707 MW; 4ACC456DE487EA93 CRC64;
E8766823D6450267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 16, Last annotation update)
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                                                                        Score 46; DB 10;
Pred. No. 4.3;
3; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 1
Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHEROMONE-RESPONSIVE MAPKK KINASE UBC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLIEL) 15, Created)
01-OCT-2000 (TrEMBLIEL) 15, Last sequ
01-MAR-2001 (TrEMBLIEL) 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                  3,
                                                                                                                                                                                    1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                         58 GKTFNLEVKGSEIIQQVKNMI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.0%;
58.8%;
                                                                             43.0%;
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Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TFQVEVPGSQHIDSQKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 43.0
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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2732 AA

PRT;

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Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.; "Pathogenesis and sequence analysis of mouse hepatitis virus type 2; an experimental model system of acute meningitis and hepatitis in
                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                     EMBL, AF208066; AAF69332.1, -.
RNA-directed RNA polymerase.
SEQUENCE 2732 AA; 309135 MW; 46D0385DE231DC49 CRC64;
                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                       RNA-DIRECTED RNA POLYMERASE. murine hepatitis virus.
                                    PRELIMINARY;
                                                                                                                                                                                                                                                            mice.";
Submitted (NOV-1999)
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=11138;
                                                                                                                                                                                                       STRAIN=PENN 97-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              039226
                                                  09J3F2
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                                    09J3F2
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039226
       RESULT
09J3F2
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                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Rieger M., Mewes H.W., Rudd Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                            SMART; SM00220; S_TKc, 1.—
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 1166 AA; 123298 MW; A89E0019AABD4172 CRC64;
MEDLINE-20331594; Pubmed=10875339;
Andrews D.L., Egan J.D., Mayorga M.E., Gold S.E.;
"The Ustilago maydis ubc4 and ubc5 genes encode members of a MAP kinase cascade required for filamentous growth.";
Mol. Plant Microbe Interact. 13:781-786(2000).
EMBL; AF197562; AAF86841.1;
InterPro; IPR00104;
InterPro; IPR00104;
InterPro; IPR001059;
InterPro; IPR001059;
                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o;
                                                                                                                                                                                                                                                                                                    3; Length 1166;
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                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI63818; CAB87801.1; -.
InterPro; IPR001752; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00129; KISC; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 439 AA; 49028 MW; 9BD55085A1966D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) KINESIN HEAVY CHAIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                    Score 45.5; DB
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pront Prof. Kinesin; 2.
PRINTS; PR0025; KINESINHEAVY.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.1%; Score 45; DB 38.1%; Pred. No. 34;
                                                                                                                                                                     PRINTS, PR00308; ANTIFREEZEI.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                    42.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                        732 QVELPSGDSHLDQRKKGM 749
                                                                                                                                                                                                                                                                                                                                                        5 QVEVP-GSQHIDSQKKAI 21
                                                                                                                               InterPro; IPR000719; -.
InterPro; IPR002290; -.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                           Query Match 4.2...
Best Local Similarity 50.09
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.1
Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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EMBL/GenBank/DDBJ databases

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                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leparc-Goffart I., Hingley S.T., Chua M.M., Jiang X., Lavi E., Welss S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.1%; Score 45; DB 14; Length 2733; 52.9%; Pred. No. 2.4e+02; Live 2; Mismatches 6; Indels
                Score 45; DB 14; Length 2732;
Pred. No. 2.4e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weiss S.R., Leparc-Goffart I., Hingley S.T.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AR029248; ARB86811; -
RNA-directed RNA polymerase.
SEQUENCE 2733 AA; 309126 WW; 41A96EB2E2316CD9 CRC64;
                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                       2733 AA
                                                         2; Mismatches
                                                                                                                                                                                                                                                                                Created)
                  42.1%;
52.9%;
                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                      RNA-DIRECTED RNA POLYMERASE murine hepatitis virus.
                                                                                                                       1197 ETFQNNVPNYQHIGMKR 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1198 ETFQNNVPNYQHIGMKR 1214
Query Match
Best Local Similarity 52.9"
                                                                                                 2 ETFQVEVPGSQHIDSQK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=MHV-A59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11138;
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16

RESULT Q9PYA2

91 GKTYSMEGPGIQDCDEHNKGL 111

21

1 GETFQVEVPGSQHIDSQKKAI

ò g 1198 ETFONNVPNYQHIGMKR 1214

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PRT; 2733 AA

PRELIMINARY;

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STRAIN-CV. ULTRA;
Regalado A.P., Vidal S., Neves A., Ricardo C.P.P.,
Rodriques-Pousada C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TremBirel. 06, Created)
01-JUN-1998 (TremBirel. 06, Last sequence update)
01-JUN-1998 (TremBirel. 16, Last annotation update)
01-MAR-2001 (TremBirel. 16, Last annotation update)
CLASS III CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons; core eudicots, Vitaceae, Vitis.
NCBI_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lupinus albus (White lupine).
Bukaryota; Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Paplilionoideae; Lupinus.
                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A); TISSUE-FRUIT;
Cassol T., Adams D.O.;
                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTATHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                            565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44.5; Di
Pred. No. 53;
2; Mismatches
                                                                                                                  Created)
                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00390; IALG.
Mendel; 26381; Vitvi;1190;26381.
InterPro; IPR000103; -
InterPro; IPR001100; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF019907; AAB70837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.6%;
58.8%;
                                                                                                                  (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GRPFIPEIPGSEHAIDS 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 41.6
Best Local Similarity 58.8
Matches 10; Conservative
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                                                                            PRELIMINARY;
                                                                                                                                                                                                                     Vitis vinifera (Grape).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                  01-JAN-1998
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049876;
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049876
                                   RESULT
022511
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                                                                                                                                                                                                                               SPECIES-murine hepatitis virus strain 2; STRAIN-MHV-2; Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.; "Pathogenesis and sequence analysis of mouse hepatitis virus type 2:
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES=murine hepatitis virus strain ML-11; STRAIN=ML-11;
Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.;
Pathogenesis and sequence analysis of mouse hepatitis virus type 2;
an experimental model system of acute meningitis and hepatitis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.; "Pathogenesis and sequence analysis of mouse hepatitis virus type 2; an experimental model system of acute meningitis and hepatitis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
RNA-DIRECTED RNA POLYMERASE.
murine hepatitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                               murine hepatitis virus, and murine hepatitis virus strain ML-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                              experimental model system of acute meningitis and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA-directed RNA polymerase.
SEQUENCE 2733 AA; 309420 MW; D04F6457578EC1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF208067; AAF66342.1; -. RNA-directed RNA polymerase. SEQUENCE 2733 AA; 309251 MW; 47049486732FBAFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF201929; AAF19384.1; -.
EMBL; AF207902; AAF68920.1; -.
                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2733 AA.
U1-MAY-2000 (TrEMBLrel. 13, Cr 01-MAY-2000 (TrEMBLrel. 13, La 01-MAR-2001 (TrEMBLrel. 16, La RNA-DIRECTED RNA POLYMERASE. ORF1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ETFQVEVPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ETFQVEVPGSQHIDSQK 18
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                                                                                                                                                                          NCBI_TaxID=11138, 123595,
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Best Local Similarity '
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9J3E8;
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09J3E8

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NAME OF THE PROPERTY OF THE PR

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Gaps

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Length 565; Indels

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Mus musculus (Mouse).
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                                                                          SEQUENCE FROM N.A.
                         SEQUENCE FROM N.A.
   NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9940;
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P97431;
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P97431
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                         Query Match 41.1%; Score 44; DB 10; Length 293; Best Local Similarity 38.1%; Pred. No. 32; Matches 8; Conservative 4; Mismatches 9; Indels
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41.2%; Pred. No. 36;
ative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sands A., Mak T.W.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF177668; AAF00915.1; -.
HSSP; P23906; 21RF.
                                                                                                         CHAIN 28 293 POTENTIAL.
SEQUENCE 293 AA; 31128 MW; DB1B21728F657F2F CRC64;
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330 AA; 37355 MW; EB02EC8B751CBD7D CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
c40H5.3 PROTEIN.
                                                                                                POTENTIAL.
      EMBL; Y16415; CAA76203.1; -. HSSP; P23472; 2HVM.
HSSP; P23472; 2HVM.
Mendel; 28297; Lupal; Chibl;28297.
InterPro; IPR001579; -. Pfam; PF00192; chitinase_2; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Glycosidase; Hydrolase; Signal.
SIGNAL.
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PROSITE; PRO0601; IRF; 1.
SMART; SM00348; IRF; 1.
NOW_TER 1 1
NOW_TER 330 A330
SEQUENCE 330 AA; 37355 WW; E
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142 GIDFDIEAGGAQHYDELARAL 162
                                                                                                                                                                                                         1 GETFQVEVPGSQHIDSQKKAI 21
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Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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HYDROLASES)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLRORY FACTOR 6.

Ovis aries (Sheep).

Butaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bovidae; Caprinae; Ovis.
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Chol Y., Spencer T.E., Bazer F.W.;
Cloning and Analysis of Ovine IRF-6 ";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
BEMBL, AP228446, AAR34782.1;
ThterPro: IPR001346;
Probom; PR00265; IRF; 1.
PRINTS; PR00265; IRF; 1.
PRODOM; PD002355; -; 1.
PROSTE; PS00601; IRF; 1.
SRART; SM00348; IRF; 1.
SEQUENCE 467 AA; 52970 MW; 21E04F749844D88F CRC64;
                                                                                                                                                         "Genome sequence of the nematode C:elegans: A platform for investigating biology."; sclence 282:2012-2018(1989). EMBL; Z81482; ca803954.2; -. SEQUENCE 374 AA, 42198 MW; 67D202886D6A7824 CRC64;
                                                                                                                                                                                                                                                                                                                                                    Query Match
41.1%; Score 44; DB 5; Length 374;
Best Local Similarity 42.1%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
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White \mathrm{S.;} submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.1%; Score 44; DB 6; 41.2%; Pred. No. 53;
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                                                                                                      MEDLINE-99069613; PubMed-9851916;
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TISSUE=15 DAY PREGNANT UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 GVEFHIWFPGQPHADEQKE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GETFQVEVPGSQHIDSQKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||: || :|| ::|: : | 273 QVKFPGPEHITNEKQKL 289
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Schulte U., Adgn V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                              Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                          STRAIN=BALB/C;
TISSUE=COLON, KIDNEY, GENOMIC DNA 129/J STRAIN (DR. J. ROSSANT);
Grossman A., Mittrucker H.W., Antonio L., Mak T.W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                   41.1%; Score 44; DB 11; Length 467;
41.2%; Pred. No. 53;
iive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.1%; Score 44; DB 3; Length 864;
42.1%; Pred. No. 1e+02;
tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A1355930; CAB91375.1;
Interpro; IRRO00542;
Pfam; PF00755; Carn_acyltransf; 1.
PROSITE; PS00440; ACYLTRANSF_C_2; UNKNOWN_1.
                                                                                                                                                                                                                   68CCAA90680FEDC8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE CARNITINE ACETYL TRANSFERASE FACC.
                                                                                                                                                                                                                                                                                                                                                                                    864 AA.
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SEQUENCE 467 AA; 53106 MW;
                                                                                                                                           Interpro; IPR001346; -.
Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INF; N.
ProDom; PD002355; -; 1.
PROSITE; PS00601; IRF; 1.
                                                                                                         EMBL; U73029; AAB36714.1; -. HSSP; P23906; 2IRF.
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                                                                                                                                                                                                                                                                                                                 273 QVKFPGPEHITNEKQKL 289
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Best Local Similarity 41.2
Matches 7; Conservative
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Best Local Similarity 42.1
Matches 8; Conservative
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                                                                                                                                 MGD; MGI:1859211; Irf6.
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                                                SEQUENCE FROM N.A.
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                        NCBI_TaxID=10090;
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SEOUENCE 8
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Q9P5Z5
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Q9SKB2
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MEDIINE-20083487; Pubmed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.E., Feldblyum T.V.,
Eujil C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome II of Arabidopsis thallana.";
Nature 402:761-768(1999).
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                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AC006533; AAD32284.1; -.
HSSP; Q63450; 1A06.
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7;
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50.0%; Pred. No. 89;
Live 3; Mismatches
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress)
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Job time: 473 sec
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Interpro; IPR001611; -.
Interpro; IPR002290; -.
Interpro; IPR003592; -.
Pfam; PF00069; pkinase; 1.
Pfam; PF00560; LRR; 4.
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Best Local Similarity 50.09
....hes 11; Conservative
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To:

Ford, Vanessa Wednesday, October 23, 2002 12:15 PM STIC-Biotech/ChemLib Sequence search 09/786648

Subject:

Please search SEQ ID Nos: 2, 3, 4, and 5.

Please include inteference searches.

Vanessa L. Ford

Biotechnology Patent Examiner

Office: CM1 8B13 Mailbox: CM1 8E12 Phone: 703.308.4735 CRFF

Point of Contact: Susan Hanley Technical Info. Specialist CM1 6B05 Tel: 305-4053 This Page Blank (uspto)